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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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-WODEL-frame+p2n.model.-DEV-xlp
-WODEL-frame+p2n.model.-DEV-xlp
-WODEL-frame+p2n.model.-DEV-xlp
-WO-Cgn2_1/USPTO_spool/US09912020/runat_25112002_091428_24247/app_query.fasta_1.647
-OB-CGNEDALI -OFMT-fastap -SUFFIX-p2n.rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cd1 -LIST-45
-UOTALIGN-120 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-UOTFWT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US09912020_@CGN_1_1_3637_@runat_25112002_091428_24247 -NCPU-6 -ICPU-3
-NOXLPXY -NOLWMPP -LARGEOPERY -LG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN TIMEOUT-30 -THREADS-1 -XARAPOP-10 -XARAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
                                                                                                     November 26, 2002, 10:19:57 ; Search time 3268 Seconds (without alignments) 4247.870 Million cell updates/sec
                                                                                                                                                                                     2393
1 MKVTLPEFERAGVMVVGDVM......FEDGCSTTNIIKKIQQDKKG 477
              GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 200000000
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AL627278 Salmonell AF165661 Salmonell AF163662 Salmonell AE013955 Yersinia AJ414144 Yersinia U32828 Haemophilus AE006127 Pasteurel AE0064313 Vibrio ch U17642 Haemophilus

AX189075 Sequence AX363670 Sequence AE000387 Escherich

To 6.61:

Description

AE005534 Escherich AP002564 Escherich

Salmonel Salmonell

U28379 Escherichia

Campyloba Mesorhizo Helicobac Sequence Caulobact

AE006022 AL139077 AP003000 AE001509

Pseudomon

Seguence

AX081559 AX374740

Helicobac

Buchnera

Buchnera

Neisseria Neisseria Neisseria Neisseria Ralstonia Burkholde Streptomy Fusobacte Aquifex a

AL646061 AF159428 AL035478 AE010481

Sequence

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ALIGNMENTS

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                                 AlavalvalGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle
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/transl_table=1
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QQMAQLARRAGAPVPULDPKGTPFERYRGAPLITPRNLSEEFAVVGKREEETIVBRGMK
LIADYELSALLVTRSEQGARLLQPGRAPLHMPTQAGBVYDVTGAGDFYGYDFATAA
GNSLEBACFFANAAAGVVVGKLGTSTVSPIELLBNAVRGRADTGFGVMTEEELKLAVAA
ARKRGEKVWTWGYDPILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDSRPVNP
LEQRMIVLGALEAVDWVVSFEEDTPQRLIAGILPDLLVKGGDYRPEEIAGSKEVWANG
GEVLVLNFEGGCSTTNIIKRIQQDKKG"
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Forsyth,R.A., Ohlsen,K.L. and Zyskind,J.W.
Forsyth,R.A., Ohlsen,K.L. and Zyskind,J.W.
Forsyth,R.A., Ohlsen, C. I. and Ohlsens in the constitution of the constitution 
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            AX189075 Sequence 276 from Patent AX189075
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Matches:
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/organism="Escherichia
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. 352 c 447 g 3
                              Bacteria; Proteobacteria; gamma
Escherichia.
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 from Patent
          AX363670.1 GI:18695784
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2393.00
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                    Escherichia coli.
Escherichia coli
Sequence 165
AX363670
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Query Match:
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Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V., Rilety,N., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F., Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J., Mau,B. and Shao,Y.
The complete genome sequence of Escherichia coli K-12
Science 277 (5331), 1453-1474 (1997)
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Batther, F.R.
Direct Submission
Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma subdivision; Enterobacteriaceae;
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Escherichia coli K12 MG1655 section 277 of 400 of the complete
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GluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyVaiVaiValGlyLysLeuGlyThr
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Escherichia coli K12
Bacteria; Proteobacteria;
Escherichia.
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AE000387.1 GI:1789431
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LELGSCPTRAVLKLANOLVSGTGLRGGSLSRAARGYHLAQGNPAREIKPTTILHVAAK
ADVEQGLEAALELALAAQWUYBELWYKGNDAARRGYHLAGCSVRHLAFGGIVPRRA
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SDSFKRFADIHLSRHAAELKSVFCQPLGDRYRDQLPRLTRDIDSILLLAGYYDPVVAQ
AWLENWGCLHAAIATGQRIETEHFRNEANNQEPFWLHSGKR"
(complement (5878 . 5902)
/note* No predicted promoter "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRTSSGILYEVDARLRPSGAAGMLVTSAEAFADYQKNEAWTWEHQALVRARVVYGDPQ
LTAHFDAVRREIMTLPREGKTLQTEVREMREKMRAHLGNKHRDRFDIKADEGGITDIE
FITQYLVLRYAHEKPKLTRWSDNVRILELLAQNDIMEEQEAMALTRAYTLRDELHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"orf, hypothetical protein"
/protein_id-"AAC7600.1"
/db_xref-"GI:178434"
/tb_xref-"GI:178434"
/translation-"MAQEIELKFIVNHSAVEALRDHLNTLGGEHHDPVQLLNIYYETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNWLRGHDMGLRIRGENGRYEMTMKVAGRVTGGLHQRPEYNVALSEPTLDLAQLPTEV
                                                                                                                                                                                                                                                            /product="adenylylating enzyme for glutamine synthetase"
/protein_id="AAC76089.1"
/db_xref="GI:1789433"
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1 REP sequence"
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/note="central position to predicted promoter: -154.5"
/bound_moiety="Fur predicted site"
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/note="central position to predicted promoter: -38.5"
/bound_molety="Fur predicted site"
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/note="factor Sigma70; predicted +1 start at 3198704"
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/note="factor Sigma70; predicted +1 start at 3198820"
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                                                                                                                                                        /note="f946; 99 pct identical (1 gap) to GLNE_ECOLI
                                                                                           function="enzyme; Proteins - translation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALQELPGHVSEDCFTAERELVRASWQKWLVEE"
complement(4584. .5885)
/gene="ygiF"
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/transl_table=11
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/note="b3055"
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                                                                                                                            modification"
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/note="REP (
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                                                                                                                                                                                                                                                                                                                                     All Submitted (13-OCT-1998) Laboratory of Genetics, University of Walsonia, 445 Henry Mall, Madison, WI 53706, USA

Walsonsin, 445 Henry Mall, Madison, WI 53706, USA

This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by Mill grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently reading frames were determined using GeneMark Software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 3032 (e-mall: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://www.genetics.uch.). Annotation of the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation assignments courtesy of Monica and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequence described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein or RNA-encoding) are now designated as gene synonymm instead of in an Entrez as gene and and products. This should allow them to be searched for in Entrez as gene and an entry of the products.
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ARKRGEKVVMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDSRPVNP
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GEVLYLNFEDGCSTINIIKKIQODKKG"
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QQMIQLARKAGVPVLIDPKGTDFERYRGATLLTPNLSEFEAVVGKCKTEEIVERGMK
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                                                                                                                                           Direct Submission
Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459
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complement(1721. .4561)
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                                                                                  3 (bases 1 to 11307)
Blattner, F.R.
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Conservative:
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                                                                                                                                                                                                            GlyValMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGlu
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                                                                                                                                                                                                                                                                                                                                     AAACGGCTGAAAGGGGATTCCCGCCCGGTAAACCCACTCGAACAGCGTATGATTGTGCTG
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U28379 U28379.1

ACCESSION VERSION KEYWORDS SOURCE

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ENTLATTLLARSARCYALTEGGORCYEHALETLTOYORLUDYTOTATREMINING
SFGFGRSHIAPAITELMRNYPELOVHFELFDROIDLVODNIDLDIRINDEIPDYYIAH
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                                                                                                                               Submitted (01-JUN-1995) Guy Plunkett, Laboratory of Genetics, Submitted (01-JUN-1995) Guy Plunkett, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA (On Feb 27, 1996 this sequence version replaced 91:882576.

This sequence was determined as part of the E. coli Genome Project (Frederick R. Blattner, director) at the University of Wisconsin-Madison. Supported by award HG00301 from the NIH Human Genome Project. The entire sequence was independently determined from E. coli MG1655; overlaps with other sequence determinations are annotated. The end of this entry overlaps though the start of the entry ECOUW67 (U18997) by 1596 bp. This entry should be considered somewhat provisional; it will be updated and merged with others at
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TRRRIAAVASWKEQRCPKPE"
                            Proteobacteria; gamma subdivision; Enterobacteriaceae;
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1. .25638
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/gene="cca"
6686. .7924
/gene="cca"
                                                                              (bases 1 to 25638)
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  Escherichia coli
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Escherichia.
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200 949 220 889 240 829 260 769 280 709 300 649 320 589 340 529 360 469 380 409

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GCTTCTCTCGGTGCTAATGCACGCCTGGTCGGGTTGACGGGCATTGACGATGCAGCGCGC
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ELASRDHVRKTVPLIQAALKESGLTAKDIDAVAYTAGPGLVGALLVGATVGRSLAFAM
BOVPAIPVHHWEGHLLAPMLEDNPPEFPFVALLVSGGHTQLISYTGIGOYELLGESIDD
AGBAFDKTAKLLGLDYPGRELSARAGGTAGRFVPFPRTDRFDLDFSFSGLKTFA
ANTIRNGTDDQTRATARLAGLDYPGLANKCKRALDGTGFKRLVAAGGVSANRTLE
AKLAEMMKKRRGEVFYARPEFCTDNGAMIAYAGMVRFKAGATADLGVSVRPRWPLAEL
                          /translation-*WKPSTEWMRYLAPLAVIAIIALLPVPAGLENHTWLYFAVFTGVI
VGIILEPVPGAVVAAVGISIIAILSPWLLFSPEQLAQPGFKFTAKSLSWAVGSFSNSV
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RGAGIIYPIIRNLPPLYOSQPNDSSSRSIGSYIMWMGIVADCVTSAIFLTAAMADNLLL
IGLMKSASHATLSWGDWFLGMLPLSILLVLLVPWLAYVLYPPVLKSGDQVPRWAETEL
                                                                                                                                                                                                                                                                                                                                                                                                     /LTANSlation="MPVIKVRENEPPDVALRRFKRSCEKAGVLAEVRREFYEKPTTE
RKRAKASAVKRHAKKLARENARRTRLY"
                                                                               QAMGPLCSREKRALGLAVGALVLNIEGGDYIDAANVOYSVVALMLLLEXISWDDIVSN
KAANNVFFWLASLITLATGLNNTGFISWFGKLLAGSLSGYSPTWVWVALIVVFYLLRY
FFASATAYTSALAPMATAAALAMPETPLPVFCLMVGAAIGLGSILTPYATGPSPIYYG
SGYLPTADYWRLGAIFGLIFLVLLVITGLLWMPVVLL"
complement (1432s. .15338)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dnaP,
                                                                                                                                                                                                                                                                                                                                                                      /product="305 ribosomal subunit protein S21"
/protein_id="AAA89145.1"
/db_xref="GI:882588"
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Matches:
Conservative:
Mismatches:
Indels:
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       /protein_id="AAA89143.1"
/db_xref="GI:882586"
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/db_xref="GI:882587"
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/transl_table=11
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/transl_table=11
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                                                                                                                                                                                                                                                               14862. .19917
/note="similar to
(ECORPSRPO)"
1576 .15791
/gene="rpsu"
15576. .15791
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/note="CG Site
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/gene="dnaG"
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15902. 174.
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DB:
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/transl_table=11
/product="glycogen biosynthesis, rpoS dependent"
/product="glycogen biosynthesis, rpoS dependent"
/pprotein_id="AAG58183.1"
/db_xref="GI:12517625"
/translation="MLMDHSLNSLNNFDFLARSFARMHAEGRPVDILAVTGNMDEEHR
                                                                        /protein_id="AAG58180.1"
/db_xref="GI:12517622"
/translation="MFIAWYWIVLIVLVVVGYFLHLKRYCRAFRQDRDALLEARNKYL
NSTREETAEKVE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
/product="3,4 dihydroxy-2-butanone-4-phosphate synthase"
/product="3,4 dihydroxy-2-butanone-4-phosphate synthase"
/protein_id="And58181.1"
/db_xref="G1:12517623"
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MILAGFKPAGVLCELTNDDGTWARAPECIEFANKHNMALVTIEDLVAYRQAHERKAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2343. .2678
/gene="24400"
/function="orf; Unknown function"
/note="Residues 1 to 106 of 111 are 86.79 pct identical to residues 9 to 114 of 116 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="putative enzyme; Not classified"
/note="Residues 1 to 204 of 204 are 99.01 pct identical to
residues 1 to 204 of 209 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAG58182.1" ·
/bc.xref="G1:12517624"
/translation="WALNYOYEETDMIDPKKIEQIARQVHESWPKGIREFGEDVEKK
IRQTLQAQLTRLDLVSREEFDVQTQVLLRTREKLALLEQRSSELEARNNSVADLQSPP
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/note="O-island #124; Region of the EDL933 chromosome not
homologous to E. coli K-12 MG1655"
complement(2713. 2919)
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/function="putative enzyme; Macromolecule synthesis,
modification: Polysaccharides - (cytoplasmic)"
/forde="Residues 3 to 68 of 68 are 98.48 pct identical to
residues 1 to 66 of 66 from Escherichia coli K-12 Strain
MG1655: B3049"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Residues 1 to 217 of 217 are 100.00 pct identical to residues 1 to 217 of 217 from Escherichia coli K-12 strain MG1655: B3041"
                                                                                                                                                                                                                                                                                                                                                                                                 /function="enzyme; Biosynthesis of cofactors, carriers:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative oxidoreductase"
/protein_id="AAG58184.1"
/note="No significant matches"
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/transl_table=11
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/gene="24402"
3182. .3796
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/gene="24400"
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/gene="24402"
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/function-"orf; Unknown function"
/note="Residues 1 to 257 of 257 are 100.00 pct identical
to residues 1 to 257 of 257 from Escherichia coli K-12
Strain MG1655: B3 04 0"
Strain MG1655: B3 04 0"
/transl_table=11
/transl_table=11
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/translation="wavPlifflingaarFigathered production"
/translation="wav
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shoo, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R. Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7 Nature, 409 (6819), 529-533 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli 0157:H7 EDL933.
Escherichia coli 0157:H7 EDL933
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                 228 GCCGGGAGTAAAGAAGTCTGGGCCAACGGTGGCGAAGTGTTGGTGCTCAACTTTGAAGAC 169
                                                                                                                                                                 /gene="Z4398"
/function="orf; Unknown function"
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complement(920. .1090)
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AE005534 AE005174
AE005534.1 GI:12517620
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89. .862
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MetLysValThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMet
                                                                                                       LeuAspArgTyrTrpTyrGlyProThrSerArglleSerProGluAlaProValProVal
               (1-477) x AE005534 (1-12088)
               US-09-912-020-325
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/product="putative membrane protein"
/product="putative membrane protein"
/product="putative membrane protein"
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VRVRFSVEDIATAAQTIGGRTLSPEDLENMUVEDKFVDALRATPAGNMTHAELGOTRENF
FRNEVSDUVEVNYRRENREDLESVSIJNFNOTSKEHFRUNNAFDAEGLFKLATGETERRF
ERNEXASDUVEVNYRRENREDLESVSIJNFNOTSKEHFRUNNAFTREDGOVTTARAGNAFAARAEMENGAANTSKTAPEGNAFKAARAEREARAGNALIAAAQDAETK
AVELIVRARAKEREARAEMQAAAIVELAEATRKKGLAEARAGNALIDAINVLSDEGTSK
FKLALLOALPAVIEKSVEDRKSIODEN KIJOVDGLNRGGTAGDANTGNVGGGNLAEQAL
SAALSYRTQAPLIDSLLNEIGVSGGSLAALFSLLTPTTPVAENVE"
/note="0-island #125; Region of the EDL933 chromosome not homologous to E. coli k-12 MG1655"
//conplement(6293: 7726)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(6293. .7726)

/gene="24405"
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/function="putative enzyme: Not classified"
/function="putative enzyme: Not classified"
/function="putative enzyme: Not classified"
/function="putation: Not 477 of 477 of 477 are 99.58 pct identical to residues 1 to 477 of 477 from Escherichia coli K-12 Strain MG1655: B3052"
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YNDSITTGHTEQALHYLNIGRLPALVVLCLAGFFGILGILLGHTCIMVWQSPLSNLF
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                                                                                                                                /function="putative membrane; Not classified"
//note="Residues 1 to 553 of 553 are 98.73 pct identical to
residues 1 to 553 of 553 from Escherichia coli K-12 Strain
MG1655: B0051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pct identical to coli K-12 Strain
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Proteins - translation and modification"
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residues 1 to 946 of 946 from Escherichia coli K-12 Strain
MG1655: B3053"
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Matches:
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/gene="glnE"
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                                                                      3838. .5499
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3838. .5499
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/gene="24403"
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                                 GlyValMetThrGluGluGluLeuLySLeuAlaValAlaAlaAlaArgLySArgGlyGlu
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Conservative: Mismatches: Indels: Gaps:

Percent Similarity: Best Local Similarity: Query Match: DB:

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/translation="MOCKDERFRTRASQLFPGLRAVASYINEHREVVLDQ
TAMETAATLATSDATVIRAIQALGFRGLRDLKRTLEQMLGPALSSERMSTTVSNLTS
DVRTAIDFVLBGHLYTCNVLSEPENHRALAQAVALLVQARQVAIFGIGASGILADYTA
RLFNTIGLPATALLATGIGLAGOLTALORGOVLIMAQKSAHREGITTLERAKRGIP
VILLTNALDSRFSKDASIVIHVPRGDERGKTPLHGTVLCLEMIVWSVASAVPQRAVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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/protein_id="BAB3733.1"
/db_xxef="GI:1356388"
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DPSKYVGSGGLVOGKYMLGITUNGAKKAHSNGOLNDTLTEVADGTLRDLGHDVRIVRA
DPSKXYGSGGLVOGKYMLSITWNAPWARAFTEKDOFFHGVGVDGVYLPFHKANQFLGM
EPLPTFIANDVIKMPDVPRYTEEYRKHLVEIFG"
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DCAAGVSFQSMAPDSIVMIEQMESIAHLEAHLQTPHMKAYSEAVKGDVLEMNIRILQP
                                                                                                                                                                                                                                           Hayashi,T.
Direct Submission
Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Genome
Information Research Center; 3-1, Yamadaoka, Suita, Osaka 565-0871,
Japan (E-mall:kenégen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
Fax:81-6-6879-2047)
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Ohnishi,M., Kurokawa,K., Makino,K., Yasunaga,T., Shinagawa,H. and
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E.coli K-12)"
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0157:H7 and genomic comparison: with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
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100 in 193 aa (Conserved in E
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72. .653
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684. .998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ECs3910"
72. .653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ECs3910"
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                                                                                                                                                                         (bases 1 to 307962)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome project.
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                                                TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete nucleotide sequence of the prophage VT2-Sakai carrying the verofcxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7 derived from the Sakai outbreak derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2001
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Ohnishi,M., Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli 0157:H7 (strain:0157:H7, sub_strain:RIMD 0509952)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comparative analysis of the whole set of rRNA operons between an enterohemorrhagic Escherichia coli 0157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655 Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (sites)
Yokoyama,K., Makino,K., Kubota,Y., Watanabe,M., Kimura,S.,
Yutsudo,C.H., Kurokawa,K., Ishii,K., Hattori,M., Abe,H., Iida,T.
Yutsudo,C.K., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (sites)
Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S.,
Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
Sasakawa,C. and Shinagawa,H.
                                                                                                                                                                                                                                                                                                                                                                        6347
                                                                                                                                                                             6587
                                                                                                                                                                                                                                                                              6706 AAAGTGGTAATGACCAACGGTGTCTTCGATATCCTACATGCCGGGCACGTCTCTTATCTG 6647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K.,
Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T.,
Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C.,
Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and
Shinagawa,H.
                                                                                                                                                                                                                                           400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460
                                                                                                           361 AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307962 bp DNA linear BCT 07-M
Escherichia coli 0157:H7 DNA, complete genome, section 15/20
AP002564 BA000007
AP002564.1 GI:13363382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441 AlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6346 GGTTGCTCGACCACTAACATTATCAAGAAGATCCAACAGGATAAAAAAGGC 6296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 GlyCysSerThrThrAsnIleIleLysLysIleGlnGlnAspLysLysGly 477
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gene

CDS

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system ATP-binding protein"

/dp.xef="d1:133391"

/db.xef="d1:13339391"

/translation="MAHNAKGOGLILDNVSAGYHKKIIVDGVSFSVPTEKMTVLVGAN

GCGKSTLLSTARVLQPMGGSILLDGKAIHEQPTKALSRRGILDGOSPLLPEGLTYVE

LYSRGRPPWONFIROMSDADAVEELAKLTGTGFRALLFYKELSGGORQRCWIAMVL

AQKTPYILLDEPTTMLDLRYQVEILELHDLTRHHCRTVVVVULHDLRFAVNYGDTLLF

LRQGKVVRVLNEGEHCTPELVKAVFDVDVHASINILTGKPFFMPFRGVEKV"
iron-siderophore transport
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Mismatches:
/product="putative ABC-type
                                                                                                                                                                                                                                                                                                                                        Matches:
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                                                                                                                                                                                                                                                                                                           Length:
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Query Match:
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// Abcordin_id="BAB3737.1"
// Ab_xref="G1:13363387"
// Ab_xref="G1:13363387"
// Laraslation="MSRIMWNGLRPLRVGKFSTLVRPKNLVLLGGLFLFAVGILIFGL
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complement(3931. .4914)
// gene="ECS3915"
// Gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MMRTGLVTVIFLALLLVGCVVYPGIGARFIAPQTVLQAFLHFEP
ANEDHNYIVERLEPRIAAGLITGASLGAVGALLQAYIRNPLGEPHIGLAGGALAVAV
ANALGLAFPVGRPLLASTGGALFLILLLSAGRSGLTPWKYTLGYALLARVY
TAAILILDEQTLLANTTWLAGDLAGQDWATLGTSAWFSLGGVVLAIYLAPSLNMLALG
INMAGGLGVSVLRTRTFLLAIALLCGAAVSTAGFTGTSAWFSLGGVVLAIYLAPSLNMLALG
IPLSACVGALLLLLAIALLAIALLCGAAVSTAGFTGFVGLLVPQIVRRLVSADLRVL
COMPIEMENT (4911. .5720)
                                                                                                                                                                                                                                                                                                  /translation="MRLFFSLLILLSFFRATEPVQVFTDDLGRKVTVPAHPKRIVSL
HDLDITIPLIELGVPPVASHGRTRPDGSHFIRSGALLTGVDFDNSSIAFIGTADIDIE
AIVAAKPDLIITEPTRNTPIERLEKIAPTVSIDHLKGGAPEIYRKLAELTGTQSQLAI
                                                                                                                                                                                                                                                                                                                                                                                   LERRYQAQINALKATLDSQXITVSVIQANGGXINVMISYHSIGRYURDAGFRFPPLIE
SIPEGGRMDVSAERLPELDADFVFATWRGDTGGKPQDELAAMEKVMPGWCQFLTACRS
GRYVLISREEAISNSFASLGLMAAQIQSQIAGRPLPEAK"
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                 /note="probable ferrichrome-binding protein, similar to
ferrichrome-binding proteins e.g. [Bacillus subtilis]
g1|585132|sp|P37580|FHUD_BACSU percent identity 27 in 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4911. .5720)
/gene="ECs3916"
/note="probable ABC-type iron-siderophore transport
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/gene="ECS3914"
complement(2885...3934)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence-not_experimental
/transl_table-11
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transporter"
                                                                                                                                                    /evidence=not_experimental
/transl_table=11
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/db_xref="GI:13363386"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative permease of transporter"
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/evidence=not_experimental
/transl_table=11
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/db_xref="GI:13363388"
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gene

CDS

24803

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24863

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40

24923

24743

100

24683

24623

120

24383

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24323

gene

CDS

24263

24203

280

260

24503

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160

24563

140

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                                                                                                                 24143
                                                                                  23783
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                                                                     24023
                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhimurium.
Salmonella typhimurium
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                           AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr
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                                                                                                                                                                                                                                                                       AlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp
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                                                                                                                                                                                                                                               salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-MAY-1999) Oriental Medicine,
Sukjang-Dong 707, Kyungju 780-714, Korea
Location/Qualifiers

    1431
/organism="Salmonella typhimurium"
/db_xref="taxon:602"
1. .71431

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Jin,U.-H., Chung,T.-W. and Kim,C.-H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 1431)
Jin, U.-H., Chung, T.-W. and Kim, C.-H.
ADP-heptose synthase (rfaE) gene of
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                GI:13383335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="rfaE"
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AF155126.1
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DEFINITION
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VERSION
KEYWORDS
SOURCE
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TITLE
JOURNAL
REFERENCE
AUTHORS
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/translation="mkvylpeperagvwvgdywlddywygpycrispeapvpvvkvn
TveerpggaanvamniaslganarlyglyglddaaralskTlaevwrcdpysypthp
Titklavlasroolirldfebgergvdpopelheringalgastaalvesdargatsv
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Othislargavvvlidprgydperstroperspeadymygreadelyergm
Liadydlsallyyrbgogwtlidprapheringspeadymygreadyvigv
Gnyllebacyfanaaagvvgklgtstyspielenavrgradfgwyrbeelrgavas
Arkreekvwmygvpfillaagtystlanark.Gdrlivavnsdastrklkgesrpvnp
Legmivlgalesvbwvvsfebdyforliagilpblivkgddyrpeelagsebwang
Gevwunbredgestymiikkigofesek"
357 c 467 g 296 t
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447
19
10
0
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Matches:
Conservative:
Mismatches:
Indels:
                         /product="ADP-heptose synthase"
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                                                                                                                                                                                                                                                                                                                                        (1-1431)
                                                                                                                                                                                                                                                                                                                  Gaps:
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2276.00
97.90%
93.91%
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Best Local Similarity:
Query Match:
DB:
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ReguonDB;
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  REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of Salmonella enterica serovar Typhimurium
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1 (bases 1 to 20604)

McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,

Latrellle, P., Courtney, L., Porwollik, S., Ali, J., Dante, M., Du, F.,

Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A.,

Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W.,

Stoneking, T., Nhan, M., Waterston, R. and Wilson, R. K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                          1021 AAAGTGGTCATGACCAACGGCGTTTTCGATATTCTGCACGCGGGCCATGTCTTTATCTG 1080
                      260
                                          780
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                                                                                                       GCTGATTACGACCTTTCCGCGCTGTTGGTCACGCGTTCCGAACAGGGAATGACGCTGCTG
                                                               GlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu
                                                                          441 AlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp
                     GlnProGlyLysAlaProLeuHisMetProThrGinAlaGlnGluValTyrAspValThr
                                 LysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyCysSerThrThrAsnIleIleLysLysIleGlnGlnAspLysLys 476
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11677609
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AE008847.1 GI:16421751
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AE008847/c
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BGVTTGVSAADRVTTVRAATKDGARPSDLNRPGHVFPLRAQAGGVLTRGGHTEATIDL
MTLAGFRPAGVLCEITNDDGFWARAPECIAFAGGHNMAVVTIEDLVAYRQAHERKAS
complement(778...783)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.

Location/Qualifiers
                                                                                                                                                                                                                                             Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.blology.gatech.edu/GeneMark/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dihydroxy-2-butanone-4-phosphate synthase (AAC76077.1);
Blastp hit to AAC76077.1 (217 aa), 96% identity in aa 1
217"
                                                                                                                                                                                                                                                                                                                                                                                                               EC numbers were kindly provided by Junko Yabuzaki and the Kyoto chryslopedia of Genes and Genomes, http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and
                                                                                                   Department of ', 4444 Forest
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1139. .1505
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                                                                                                                                Medicine,
                                                                                                   Center,
                                                                                                                                                                                     Supported by NIH grant 5U 01 A143283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .20604
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                                       Sequencing
2 (bases 1 to 20604)
The Salmonella typhimurium Genome Sequenci
Direct Submission
Submitted (29-MAR-2001) Genome Sequencing
Genetics, Washington University School of
Park Boulevard, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to E. coli 3,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(116. .769)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(116. .783)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="STM3195"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="ribB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene-"ribB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="LT2"
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                                                                                                                                                                                                                                                                                                                                                 QTMISLARQAGVPVLIDPKGTDFERYRGÄTLLTPNLSEFEAVAGKCKSEDELVERGMK
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LEQRMIVLGALESVDWVVSFEEDTPQRLIAGIILPDI.LVKGGDYKPEEIAGSEEVWANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="putative RBS for rfaE; RegulonDB:STMS1H003231" complement(6305. .9163)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 LeuSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerVal 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="regulates P-II (GlnB) and GlnK; similar to E. adenylylating enzyme for glutamine synthetase (AAC76089.1); Blastp hit to AAC76089.1 (946 aa), 87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 ValLysValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AlaSerLeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspASpAlaAlaArg
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445
19
12
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEVMVLNFEDGCSTTNIIKKIQTESEK"
complement(6264. .6269)
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-912-020-325 (1-477) x AE008847 (1-20604)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(6305. .9148)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="glnE"
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2265.00
97.48%
93.49%
94.65%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="glnE
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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  CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="putative RBS for STM3198; RegulonDB:STMS1H003229"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2671. .4364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anote-"similar to E. coli putative membrane protein (AAC76087.1); Blastp hit to AAC76087.1 (553 aa), 928 identity in aa 1 - 553"
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                                                                                                                                  complement(1579. .1788)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4824..6269)
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2033, ,2020
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                                                                     gene
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RBS

CDS

RBS

CDS

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VLDATTILYDARQOLANARTYLINOLNIKYALGENSONSONSONRGNFTIVD
VLDATTILYDARQOLANARTYLINOLNIKYALGENSONSONRGNFTIVD
                                                                            Salmonelia.

I (bases 1 to 258050)

Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D.,
Waln, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G.,
Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T.,
Connerton, P., Cronlin, A., Davis, P., Davies, R.M., Dowd, L., White, N.
Farrar, J., Feltwell, T., Hanlin, N., Haque, A., Hien, T.T., Holroyd, S.,
Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P.,
Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J.,
Stevens, K., Whitehead, S. and Barrell, B.G.
Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18

L. Nature 413 (6858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Orthologue of E. coli ygiB (YGIB_ECOLI); Fasta hit to YGIB_ECOLI (234 aa), 97% identity in 223 aa overlap. Contains a possible N-terminal signal sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="STY3364"
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                              Salmonella enterica subsp. enterica serovar Typhi.
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Salmonella enterica subsp. enterica serovar
Typh1"
                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Details of S. typhi sequencing at the Sanger Centre to the World Wide Web.
(URL, http://www.sanger.ac.uk/Projects/S_typhi/).
Location/Qualifiers
1. .258050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref-"taxon:90370"
                                                                                                                                                                                                                                                                                                                                                                                                                        E-mail: parkhill@sanger.ac.uk
Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="STY3364"
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69. .1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1757. .2428
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Parkhill,J.
Direct Submission
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REFERENCE
AUTHORS
TITLE
JOURNAL
                                                  ORGANISM
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                                                                                                REFERENCE
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 VERSION
KEYWORDS
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                                                                                                                                                                                                                                           TITLE
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                                SOURCE
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                                                                   GlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr
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/translation="MFDQYRKTILAGAVALTCGLTAASTFAAGFQPAQPAGKLGAVVV DFYGNALTALVELDSHILSDKVYVYHGKGBKGPVYYYVDSTKGSLEFYDOIPFFGLYQ DFYGNALVELVSHYKOVPYTYVEVENGSEFEYDGLYFFGLYQ LVANTYTEYEVGAGEFHWHGEKDKNAGILDAGPAGGALPFDIAPYTFVVDTGGEFRWHLD LVNTHTFTPQGAEFHWHGEKDKNAGILDAGPAGGALPFDIAPYTFVVDTGGEFRWHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                      QDTFYNGHDMNINKRGYLMGIRETPRGTFTAVQCQHWYEFDMMGQILADHKLPRGFLD
ARBESIETWOGTVLLRVGKRDKRREDGTHWHTLPQIIEDWBGSRVVDWDLYKLIDP
MRDALLGALDAGAVCWVDLAHAGQOAKLEPDTFYGDALGYOGAGRWAHWYDAYDAK
DDSIILSSRHQGIVKIGRDKQVKWILAPSKGWNRQLASKLLKPVDDHGKPLTCDENGK
CKDTDEDPTYTOHTAWLSSKGTYLTVPDMGDGRCIBQPALPTMKYSRFYEKKIDEKKGT
VQQVWBYGKERGYDFYSPITSVVEQKORDPHRGFGGGSINLFDVGKFTVGKLDDKK
TKEVKVELDVLSDKFNQTHYRALLVHPTQMFK"
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IAKDKAAGISLFDAKSQFKKAKFAWYTAYHDKKERWSDGKDPAAFIKTGLDAAGMSQA
DFEAALKDPAVQETLEKWKAAYDVAKIQGVPAYVVNGKYLIYTKNIKSIDSMAELVRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:Q823N5"
/translation="MSSKWITSLFKSVVLTAALVTPFAASAFTEGTDYMVLEKPIPNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="51..."
/note="613371"
/gene="STY3371"
/gene="SIMilar to Enterobacter amnigenus disulfide
/note="Similar to Enterobacter amnigenus disulfide
isomerase dabA TR:09XDP1 (EMB::AF(1.2826) (222 aa) fasta
'~~a: E(): 0, 90.1% id in 222 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Similar to Klebsiella pneumoniae arylsulfate
sulfotransferase assT TR:P97036 (EMBL:U32616) (598 aa)
fasta scores: E(): 0, 86.8% id in 598 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
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                                                                                                                                                                                                                                  /product="probable arylsulfate sulfotransferase"
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oxidoreductase, score 12.90, E-value
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                          /protein_id="CADD07717.1"
/db_xref="G1:16504269"
/db_xref="SPTREMBL:Q8Z3N6"
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/product="disulfide isome
/protein_id="CAD07718:1"
/db_xref="GI:16504270"
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/gene="STY3371"
/note="Pfam match to
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/gene="STY3372"
/note="dsbB"
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/gene="STY3371"
                                                6004. .7800
/gene="STY3370"
/gene="STY3370"
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Best Local Similarity:
Query Match:
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//translation="MSVPLITLLLAGATEIGAFLGYLGQRPSNRVLAFSLGFAAGIM
//translaticsecomsvvlgycomfilellgyfgred.pratavalhniPeglavagpv
GSIRRTAILLTLGISLHNFPEGIATFVTASSNLELGFGIALAVALHNIPEGLAVAGPV
STATGSRRTATFWAGISGMAETLGGYLAWLILGSLVSPIVMAAIMAAVAGIMVALSVD
ELMPLAKETDANNNFSYGVLGGMSIMGLSLVILQTIGIG"
6004. 7800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_teable=11
/product="conserved hypothetical protein"
/protein_id="CAD07714.1"
/protein_id="CAD07714.1"
/protein_id="CAD07714.1"
/db_xref="SPTEREME.:QBYFP6"
/translation="MERVSITERPDWRDKATEYGFNFHTMYGEPYWCEDAYYKLTLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEKLEDVTAELHQMCLKVVERVIASDELMTKFRIPKHTWGFVRQSWOTQQPSLYSRLD
LAMDGIGEPKLLENNADTPTSLYEAAFFQWIWLEDQINAGNLPEGSDQFNSLQEKLIE
RFAELREQYGFQLLHLTCCRDTVEDRGTIQYLQDCAAEAEJATEFLYIDDIGLGEKGQ
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FPDHENLLPAYFAEDEHPPWDKYVVKPIFSREGANVSIIENGKTIESVEGPYGEEGMI
VQQFYPLPKFGDSYTLIGSWLINDQPAGIGIREDRALITQDLSRFYPHIFVEG"
complement (3659, .4489)
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AQRLVELLAPPPVALDKEAWGFDHGSWGVLIKMYPNADIPWYQLSYDSTKPAAWHFEM
GRKLATLRDBGVMLVASGWYVNILRTVWHGDNI PYPWAASFNDFVKANLTWGGPVEG
HPLWYRLQHEGGALDSRPTPEHFLDLIVVLGANOGKEPTITPVDGIEBMSSISMLSSVQVG
                                                                                                                                                 SLYONADDCSAANPGKSAECTTAYNNALKEAERTAPKYATREDCVAEFGEGOCOOAPA
QAGMAPENQAQAQQSSGSFWMPLMAGYMMGRLMGGGAGFAQQPLFSSKNPASPAYGKY
TDAAGKNYGAAQPGRTMTVPKTAMAPKPATTTTVTRGGFGESVAKQSTWQRSAAGTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
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/protein_id="cab07715.1"
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/db_xref="sprexbel.0857"
/db_xref="sprexbel.0857"
/tb_xref="sprexbel.0857"
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                                                                                                                           /translation="MKRTKSIHHASFRKSWSARHLTPVALAVTAVFMLAGCEKSDETV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Orthologue of E. coli ygiE (YGIE_ECOLI); Fasta hit to YGIE_ECOLI (257 aa), 93% identity in 257 aa overlap.
Contains multiple possible membrane spanning hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Orthologue of E. coli ygiD (YGID_ECOLI); Fasta hit
to YGID_ECOLI (271 aa), 87% identity in 266 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="Fasta hit to YJFC_ECOLI (387 aa), 50% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ء</u> ب
                                                                                                                                                                                                                                                                               /gene="STY3365"
/note="PS00013 Prokaryotic membrane lipoprotein lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sta hit t
overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Orthologue of E. colinygic (YGIC_ECOLI); Fasta YGIC_ECOLI (386 aa), 94% identity in 386 aa ove
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/protein_id="CAD07713.1"
/db_xref="G1:16504265"
                                                                                              /db_xref="SPTREMBL:Q8XGZ1"
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/db_xref="G1:16504268"
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/gene="STY3367"
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/gene="STY3366"
2434. .3507
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/transl_table=11
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/gene="STY3368"
4588. .5361
/gene="STY3368"
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/transl_table=11
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/gene="STY3366"
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1030. .1431
/gene="rfaE"
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Valvano, M.A.
                                                                                                                     Salmonella enterica
Salmonella enterica
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AF163661
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                                                            GlyAlaLeuGluAlaValAspTrpValValSerPheGluGluAspThrProGlnArgLeu
                           AlaLeuSerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThr
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Valvano, M.A., Marolda, C.L., Bittner, M., Glaskin-Clay, M., Simon, T.L. and Klena, J.D.
The riag gene from Escherichia coli encodes a bifunctional protein involved in biosynthesis of the lipopolysaccharide core precursor
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Submitted (28-JUN-1999) Micorbiology and Immunology, University
Western Ontario, DSB3003, London, Ontario N6A5C1, Canada
Location/Qualifiers
Enterobacteriaceae;
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of ADP-glyceromannoheptose"
/note="putative ADP transferase"
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J. Bacteriol. 182 (2), 488-497 (2000)
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/organism="Salmonella en/strain="SL1027"
/db_xref="taxon:28901"
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AF163661
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/gene="rfaE"
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1. 1434
/gene="rfaE"
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Conservative:
Mismatches:
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Gaps:
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Salmonella enterica.
Salmonella enterica
Bacteria; proteobacteria; gamma subdivision; Enterobacteriaceae;
Bacteria; proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.

1 (bases 1 to 1464)
Valvano, M.A. Marolda, C.L., Bittner, M., Glaskin-Clay, M., Simon, T.L.
and Klena, J.D.
The riag gene from Escherichia coli encodes a bifunctional protein
involved in biosynthesis of the lipopolysaccharide core precursor
ADP-L-glycero-D-manno-heptose
J. Bacteriol. 182 (2), 488-497 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                       1464 bp DNA linear BCT 12-JAN-2000 enterica RfaE mutant (rfaE) gene, rfaE-543 allele,
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            LysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeu
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complete cds.
AF163662
AF163662.1 GI:5734095
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Valvano, M.A.
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AF163662
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Deng,W., Burland,V., Plunkett,G. III, Boutin,A., Mayhew,G.F.
Liss,P., Perna,N.T., Rose,D.J., Mau,B., Zhou,S., Schwartz,D.,
Fetherston,J.D., Lindler,L.E., Brubaker,R.R., Plana,G.V.,
Straley,S.C., McDonough,R.A., Nilles,M.L., Matson,J.S.,
Blattner,F.R. and Perry,R.D.
Genome Sequence of Yersinia pestis KIM
J. Bacteriol. 184 (16), 4601-4611 (2002)
                                                                                                                                                                                                                                          LysArgLeuiysGlyAspSerArgProValAsnProLeuGluGlnArgMet1leValLeu
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Yersinia pestis KIM section 355
AE013955 AE009952
AE013955.1 GI:21960480
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Yersinia pestis KIM
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AUTHORS
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/protein_id="Aad49847.1"
/db_xref="G1:5734096"
/translation="RNNUEARERACWAVGDVMLDRYWYGPTCRISPEAPVPVVKVN
/translation="MRNUEARERACWAVGDVMLDRYWYGPTCRISPEAPVPVVKVN
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TTTKLRVLSRNOQLIRLDFEBTRGGTLTGIDDAARALSKTLAEVNVKCBFUSVPTHP
TTTKLRVLSRNOQLIRLDFEBTRGGTLTPINLSEFBTVAGKCKSEDELVERGMK
LIADYDLSALLVTRSEQEMTLLQPNKAPLHMPTQAQEVYDVTGAGDYVTGYLAAGNTL
ERACYFANNAAGVVVGKLGTSTVSPLELENNYRGRADTGFGYWTEBELRQAVASARKR
GERYVWTNGVFDILHAGHYSTLANRRLGDRLIVANSDASTKRLKGESRPVNPLEQR
MIVLGALESVDWVVSFEEDTPQRLIAGILPDLLVKGGDYKPEEIAGSEEVWANGGEVM
VLNFEDGCSTTNIIKKIQTESER"
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/note="deletion o
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/note="glycine t
/replace="g"
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/note="residues 1 to 77 of 93 are 90.90 pct identical to residues 21 to 97 of 116 from E. coli K12: B3042; residues 1 to 82 of 93 are 89.02 pct identical to residues 13 to 94 of 111 from GenPept: >psi | A5658182.1| AE005534) z4400 gene product | Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative transport"
/product="putative transport"
/brotein.id="AAM87071.1"
/db.xref="81:21980408."
/translation="MAVGGLKQELSIAQGVGLLSTSLLGTGVPAVPALAAMLAGHDSL
WAMPVLIVLFPIATAFAALGRHFPSAGGAAHFVAIAFGPKLGKVTGWLFLSYIPVGL
PAALQIAAGFWQAMFGWSDTGLLMYQUTALLVIMLLGTRSAGSANLQTYTALLVIAL
VAAIWWGGDIRLSQIPWPALQDVSPPNIFNLAVWFWCFVGLEAFAHLATEFRHPERD
FPRALIVGLLVAGAVYWGCTVAVLHFQAYGESQAAAASLPGIVVQLFGEHALMIACII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MGGKCMKVTLPDFRRACVLVVGDVMLDRYWYGFTCRISPEAPVP
VVKVDTIEEREGAANVAMNASLGAVARLVGLTGIDDAARALICKLSEPRVRCDFVS
VVKVDTIEEREGAANVAMNIASLGAVARLVGLTGIDDAARALICKLSEPRVRCDFVS
VPTHTTKLRVLSRNQOLILIDFEEGFDGVDFTFFFROLALPOIGALVLSDYAKG
ALNSVQPMIQLARKANVPVLLDPKGSDFERYRGATLLPNLSEFEAVVGRCKNEEELV
NRGMQLVADFELSALVYTRSEQGMTLLQLGKPPLHLPTQAKEVFDVTGAGDTVIGVLA
AALAGNGSTESCFLANAAGVVVGKLGTSTVSPIELBNATRGRAETGFGVMDEQQLK
INAVQARAGVGSKVVWTNGIFDILHAGHYSTLANARKLGDRLIVAVNSDASTKRLKGER
RPVNPLEQRMVVLGALEAVDWVVPFEEDTFORLIADILVAGGDYKPHEIAGSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="putative transport"
/note="residues 3 to 413 of 418 are 70.07 pct identical to residues 1 to 411 of 418 from E. coli K12 : B4141"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GYLACFASVNIYTQSFARMVWSQSQVRPQSKLÄRLSAGGTPVNALTAVVGSCLVFALL
IYWLALPLDLLIVYANGIFVLIYLLCMLAGIRLLSGRARVMSVIGSLLCCVLLVMIGW
KSVYALLMFALLWMLMSKRYTQLTQP"
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/product="adenylylating enzyme for glutamine synthetase"
/protein_id="AAM8/073.1"
/db_xref="GI:21960487"
/translation="MRRGYKESDMLPLPSELQIQAQSIKQRFSELPAPPDLRDEDIAV
                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MIDPKKIEQIARQVHESWPKGIREFGEDVEKKIRLILQSQLTRL
DLVNNEEFDVQTQVLLRTREKLALLEQRVGALEAKFNSAPADHGEKTGE"
complement(3269. .4525)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 481 are 86.10 pct identical to from E. coli K12 : B3052"
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RRRVWVRIAWSQVLQTSGTAETLQQLSTLAESMIIAARDWLYQVCCRELGTPCNRQGV
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complement(6121. .9003)
                                                                                                                                                                                                                                                                                                                        protein"
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/product="putative kinase"
/protein_id="AAM87072.1"
/db_xref="G1:21960486"
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                                                                                                                                                                                                                                                                                        /transl_table=11
/product="hypothetical p
/protein_id="AAM87070.1"
/db_xref="GI:21960484"
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/gene="y3524"
complement(4556..6001)
/gene="y3524"
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/product-hypothetical protein"
/product-hypothetical protein"
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VASGNVVHNLRLGKWQGESSPYPWAESFNQFVRDLSXQGDDHPLVNFWQHEGAALSN
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/protein_id="aam87069.1"
/d_xxef="fg1:21960483"
/translation="warshreningshppy.plfskroprowlfsfpolaysckhlri
FVWTNAPHLEIYRCISPADTVTLSHPDYNRRPRNYTGSADLYLALLDKRNNWSARGLL
HHRRDYIVAIQFTAGGDFHPALRISPWTIALLIHLGNYQNAELNASRGLYNOHRALY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"3,4 dihydroxy-2-butanone-4-phosphate synthase"
protein_id="AAM87068.1"
/db_xref="GI:21960482"
/translation="MNQTLLSDFGTPVERVERAIDALRNGRGWMVLDDESRENEGDMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAAEAMTLEOMALTIRHGSGIVCLCITDERRQOLDLPWMVTHNSSQFQTAFTVTIEAA
EGVTTGVSAADRLTTIRKAIADNAKPADLNRPGHVFPLRGQPGGVLSRRGHTEASIDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement(234. .1016)

'gene="y3519"

complement(234. .1016)

'gene="y3519"

'note="residues 1 to 260 of 260 are 70.99 pct identical residues 10 to 271 of 271 from E. coli K12: B3039;

residues 10 to 271 of 271 from GenPept: B3039;

residues 10 to 271 of 271 from GenPept: Agentical to 260 of 260 are 72.13 pct identical to 271 of 271 from GenPept: protein [Escherichia coli 0157:H7 EDL933]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ribb"
/function="enzyme; biosynthesis of cofactors, carriers:
                            2 (bases 1 to 10641)
Deng,W., Burland,V., Plunkett,G: III, Boutin,A., Mayhew,G.F.,
Liss,P., Perna,N.T., Rose,D.J., Mau,B., Zhou,S., Schwartz,D.C.
Fetherston,J.D., Lindler,L.E., Brubaker,R.R., Plana,G.V.,
Straley,S.C., McDonough,K.A., Nilles,M.L., Matson,J.S.,
Blattner,F.R. and Perry,R.D.
Direct submission
Submitted (21-FEB-2002) Genetics, University of Wisconsin, 445
Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSPEHYLPLLYVLGSWDGKEPVSIPTDGVEMGSLSMLSVQIG"
                                                                                                                                                                                                                                                                                                                                                                 /organism="Yersinia pestis KIM"
                                                                                                                                                                                                                                                                                                                                                                                                    /strain="KIM"
/db_xref="taxon:187410"
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2145. ">2527
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PQPLLILGMGKLGGGELNFSSDIDLIFAYPENGOTGGRRELDNAQFFTRLGGRLIKA
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TMRDEIHHLALQEGSSKVAADSFILEREQVAASWHKWLAANDANVS"
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complement(9285..10466)
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residues 1 to 386 of 433 from E. coli k12 : B3054;
residues 1 to 386 of 433 from GenPept : >emb[cAD07727.1]
(AL671278) conserved hypothetical protein [Salmonella enterica subsp. enterica serovar Typhi]"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                           US-09-912-020-325 (1-477) x AE013955
               Percent Similarity:
Best Local Similarity:
Alignment Scores
Pred. No.:
                          Query Match:
DB:
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               GlyValMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGlu
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|GGGTGATGGATGGATGGAGCAGCTGAAAATAGCGGTTGCGCAGCCTGGCGAGGGTGAGGAG
                                                                                                                                                                                                                                         GluGluAlaCysPhePheAlaAsnAlaAlaGlyValValValGlyLysLeuGlyThr
                                                                                                                                                                                                                                                               AlaValValGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle
                                                                                                                             GlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr
                                                                                                                                    LysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeu
                                                                                                                                                                                                                                                                                                                                                        AlaGlySerIysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp
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2730. 3089 //
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   typhimurium 30S ribosomal protein S21 RpsU SW:RS21_ECOLI (P02379) (70 aa) fasta scores: E(): 2.3e-27, 100.0% id in 70 aa, and to Buchmera aphidicola (subsp Acyrthosiphon pisum) 30S ribosomal protein S21 RpsU TR:BAB12780 (EMBL:APQ01118) (71 aa) fasta scores: E(): 1e-25, 90.1% id
                                                                                                                                                                                                               Parkhill, J., Wren, B.W., Thomson, N.R., Titball, R.W., Holden, M.T.G., Prantice, M.B., Sebaihia, M., James, K.D., Churcher, C., Mungall, K.L., Baker, S., Basham, D., Bentley, S.D., Brooks, K., Cerdeno-Tarraga, A.M., Chillingworth, T., Cronin, A., Davies, R.M., Davis, P., Dougan, G., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Karlyshev, A.V., Moulle, S., Oyston, P.C.F., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Genome sequence of Yershia pestis, the causative agent of plague Nature, 413 (6855), 523-527 (2001)
BCT 06-JUN-2002
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                                                                                                                                             Versinia pestis
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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/note="Pfam match to entry PF01165 Ribosomal_S21,
Ribosomal protein S21, score 127.90, E-value 1.9e-34"
/gene="YPO0645"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (04-0cr-2001) Submitted on behalf of the Yersinia
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
Hinxton, Cambridge CBIO 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(92. .307)
/gene="YPO0645"
/note="Identical to Escherichia coli and Salmonella
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  linear
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  DNA
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208050 bp
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                                                                    AJ41414.1 GI:15978734
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Parkhill, J.
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aldolase Folb SW.FOLB_ECOLI (P31055) (122 aa) fasta
scores: E(): 0, 84.7% id in 118 aa, and to Vibrio cholerae
putative dihydroneopterin aldolase VC0524 TR:09KUJ6
(EMBL.ABO04138) (129 aa) fasta scores: E(): 2.9e-30, 67.2%
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82.8% id in 204 aa, and to Haemophilus influenzae
hypothetical protein H10266 Sw.rGTH_HAEIN (P44602) (199
aa) fasta scores: E(): 0, 67.3% id in 199 aa" **AAGEAFDKTAKLLGLDYPGGPMLSRMAQQGTVGRFTFPRPMTDRPGLDFSFSGLKTFA** ANT IRANGDDDGTRADIARAFEDAVVDTLAIKSKRALDQTGFKRLVIAGGVSANQTLR LKLADMMQKRGGEVFYARPEFCTDNGAMIAYAGMVRLRSNLNSELSVSVRPRWPLSEL predicted transmembrane helices predicted (P05852) (337 aa) fasta scores: E(): 0, 87.8% id in 335 /gene="YP00646" /note="Pfam match to entry PF00814 Peptidase_M22, Glycoprotease family, score 649.20, E-value 2.2e-191" /gene="YPO0646" /note="PS01016 Glycoprotease family signature." complement(1972. .2622) /gene="YPO0647" transmembrane helices /transl_table=11
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complement(2545. 2610)
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                                                                                                                                                 TITGAAGAGGCTITGACGCTGTTGATCCCACGCCGATATTCGAGCGCATTCAACTGGCG 11629
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                                                                                                  AlaLeuSerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThr 100
                                                                                                                                                                                                                                                                                                      GlnGlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGly 180
                                                                                                                                                                                                                                                                                                                                                                                                         AlaValValGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle 220
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                                                 AlaSerLeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAlaAlaArg
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Bacillus subtlish yppothetical protein YubB TR:P94507
(EMBL:Z99119) (276 aa) fasta scores: E(): 0, 47.5% id in
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92.84%
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// Organism="Haemophilus influenzae

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                                                FEATURES
    COMMENT
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Rirkness, E.F., Kerlavage, A.B., Bulte, C.J., Tomb, J., Dougherty, B.A.,
Merrick, J.M., McKenney, K., Sutton, G.G., FitzHugh, W., Fields, C.A.,
Gocayne, J.D., Scott, J.D., Shirley, R., Liu, L.I., Glodek, A.,
Kelley, J.M., Weldman, J.F., Phillips, C.A., Spriggs, T., Hedblom, E.,
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Geoghagen, N.S., Gnehm, C.L., McDonald, L.A., Small, R.V., Fraser, C.M.,
Smith, H.O. and Venter, J.C.
Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U32828 14465 bp DNA linear BCT 29-MAY-1998 Haemophilus influenzae Rd section 143 of 163 of the complete
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The H. influence sequence has been updated by R. Fleischmann. New database matches have been assigned, product names have been database matches have been sittle have been corrected. We gratefully acknowledge the work of Tatusov et. al. We have incorporated their amountation into the /notes fields of the
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12410 GGTGCGTTGGAAGCGGTGGATTGGGTCGTGCCTTTGAAGAAGATACGCCACAGCGTTTA 12469
                                                                                                                                                                                                                                                                                                                                            Submitted (28-MAY-1998) The Institute for Genomic Research, 9712
                                                                                                                                                                                                             12470 ATTGCTGATATTTTGCCCGATCTGTTAGTCAAAGGCGGCGATTATAAGCCCCCATGAAATT 12529
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Tatusov, R.L., Mushedian, A.R., Bork, P., Brown, N.P., Hayes, W.S., Bordovsky, M., Rudd, K.E. and Koonin, E.V.
Metabolism and evolution of Haemophilus influenzae deduced from whole-genome comparison with Escherichia coli
Curr. Biol. 6 (3), 279-291 (1996)
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The whole genome was shifted by 588 nucleotides for a new start
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                                                                                                                                                        GlyProThrSerArgIleSerProGluAlaProValProValValLysValAsnThrIle 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluPheGluArgAlaGlyValMetValValGlyAspValMetLeuAspArgTyrTrpTyr
                                                                                                                                                                                                                                                                                                                                                                               6304 CGTGGGGCTACATTATTGACACCCAATATGTCTGAATTTGAAGCTGTTGTGGGTAAATGC
                                                                                                                                                                                                                                                            AlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||||| ::: ||||||| AATGTAGAAGTTAGAAAGTGCGGTGAAAAATTACGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgG1yAlaThrLeuLeuThrProAsnLeuSerG1uPheG1uAlaValG1yLySCys
                                                                                                                                                                                                         GluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsn
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             Conservative:
Mismatches:
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                                                                            (1-14465)
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AKARGEKIYWTNGCPDILHPOHYSYLENARKLGDRIYAVNSDDSYKRLKGFPPIND
LQSRMAVLAGLSSVDWLVAFHEDTPQRLIAEVLPDLLVKGGDYKPEDIAGSQEVWASG
GDVKVLNFENGCSTSNVISKIQQLKD"
1892. .2833
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/gene="PM0885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLGWLLAKSTVGQRRANIARRNLQLCFPHYSADQIETLLHANLKATGWAITETGWAWF
SADATKWRSKIEGLEYLKEYKQDGYJLVGYHFLTLELGARLYGLHQFGIGYYRPUDN
PLMDWLQVQGRLRSNKDLLDRKDLKGMTRALRQGEIIWYAPDHDYGRKNAVFYFFAV
PDAATTTGSYYLLKSSPTSKVIPFABLNSDGSGYTWKISPFVDFSDITDETRIATRM
NQVVETEIMKGVEQYWWLHRRFKTRPDENQPSLYDEE"
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Iwaleldnosogainsvompldlaniskeydkifwgdfpovstkisdyavsveefvnf
Roorgmpalesadhfallitaswiednidsyaaghqleegfellpcasofftqveska
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complement(4117. .4566)
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GRSFEEACYLANVAAGIVVGKLGTSTVSTVELENAIHGRSNTGFGIMSEAELKRVVAQ
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FTLTBOSLBTUON="MDFINGLPIATIFFIVLVIFVLXSTLKTVPQGYHWTIEREGRYT
FTLTPGLNTVVPFIDRYGRRINMMEQYLDIPSQEVISKDNANYSIDAVCFVQYIDARN
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/gene="PMO886"
complement(2932. .3507)
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/gene="PM0887"
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/gene="PM0887"
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/product="unknown"
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Pasteurella multocida PM70 section 94 of 204 of the complete
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St. Paul, MN
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Pasteurella.
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GluLeuLysLeuAlaValAlaAlaArgLysArgClyGluLysValValMetThrAsn
                                      GlyAspArgLeuIleValAlaValAsnSerAspAlaSerThrLysArgLeuLysGlyAsp
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                                                                                                                               347 GlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeu
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Submitted (24-OCT-2000) Department of Veterinary
University of Minnesota, 1971 Commonwealth Ave.,
55108, USA
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/organism="Pasteurella
/strain="PM70"
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/gene="rfaE"
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complement(238. 1668)
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1. .10747
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AE006127.1 GI:12721196
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Zhang, Q. and Kapur, V.
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BASE COUNT ORIGIN

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Search completed: November 26, 2002, 22:04:32 Job time : 3572 secs

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1 MKVTLPEFERAGVMVVGDVM......FEDGCSTINIIKKIQQDKKG 477
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                        908470 seqs, 133250620 residues
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A_Geneseq_101002:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
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7	2393	100.0	477	22	AAU34708	E. coli cellular p
e	2393	100.0	477	22	AAG98421	Escherichia coli p
4	2265	94.7		22	AAU38166	. Salmonella typhi c
5	1350.5	56.4		22	AAU36486	Pseudomonas aeruqi
9	745.5	31.2		23	AAU72936	Neisseria meningit
7	734.5	30.7	424	18	AAW20763	H. pylori cytoplas
æ	610.5	25.5		21	AAB07577	Protein encoded by
σ	197	8.2		22	AAU36261	Pseudomonas aerugi
10	191.5	8.0		22	AAU35299	Enterococcus faeca

Carr GJ;

Putative P. abyssi Herbicidally activ Haemophilus influe Human ORF2164 prot E. coll cellular p Escherichia coli p Salmonella typhi c Stankulococus	Standburger state Salmonella thalia Arabidopsis thalia Arabidopsis thalia H. pylori cytoplas E. coli cellular p Novel human diagno	idermidis dopsis the dopsis the polypepti transfere	S S T T T S S S S S S S S S S S S S S S	Drosophila melanog Staphylococcus aur Staphylococcus aur Staphylococcus aur Staphylococcus aur Arabidopsis thalia
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ALIGNMENTS

RESULT 1 AAB15968 XX AC AAB15968; XX C C C C C C C C C C C C C C C C C C	WPI; 2000-5148 N-PSDB; AAA659 Novel polynucl proliferation,
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                                     AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide sequences derived from Escherichia coli which inhibit E. coli proliferation. AAA65809 to AAA66055 and AAB15806 to AAB16040 represent nucleotide and protein sequences associated with E. coli proliferation. AAA66057 represent primers used for sequencing E. coli proliferation inhibiting nucleotide inserts in an example from the present invention can be used to identify a proliferation. Methods from the present invention can be used to identify a proliferation-required gene in a microorganism, by contacting a microorganism with a proliferation-required gene activity inhibitory inhibition occurs in the second microorganism, and determining if inhibition occurs in the second microorganism. The nucleic acid sequences identified as being required for bacterial growth and proliferation, can be used for antisense therapy for killing bacteria.
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                                                                                                                                                                                                                                                                                                 121 FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 180
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                                                                                                                                                                                                                                                         MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI 60
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                                                                                                                                                                                                       Score 2393; DB 21; Length 477; Pred. No. 4.2e-208; Indels 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
 for use in antisense therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E. coli cellular proliferation protein #289.
                   Claim 11; Page 242-243; 316pp; English.
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aucus, Salmonella typhi, Klebsiella penumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used in dentify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is also useful to screen casential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                        Carr GJ;
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                                                                                                                                                                                                                                                                                                                                                                        Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                     Wall
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Xu HH;
                                                     ; 2000US-191078P.
; 2000US-206648P.
2000US-207727P.
; 2000US-242578P.
; 2000US-253625P.
; 2000US-253625P.
21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                                                                                                  (ELIT-) ELITRA PHARM INC
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Matches 477; Conserv
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                                                                                     23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a purified or isolated nucleic acid sequence (1) consisting essentially of one of the 93 nucleotide sequences sequence (1) consisting essentially of one of the 93 nucleotide sequences yiven in AAM81202 to AAM81294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism. (I) have antibacterial and antibiotic activities, and can be used in of the microorganism, inhibits proliferation of the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as diagnostic tools.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. AAHB1195 to AAHB1197 encode the Escherichia coli proteins given in AAG98239 to AAA98431, and AAHB1488 to AAHB1491 represent oligonucleotides, which are used in the exemplification of the
420
                                                                 Novel nucleic acids encoding proteins required for Escherichia coli
proliferation, useful for screening for antimicrobial agents -
                                                                                                                               Escherichia coli; identification; proliferation; microorganism; antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis; bacterial growth inhibition.
                                                                                                              IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQDKKG 477
                                                ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL
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Pred. No. 4.2e-208;
                                                                                                                                                                                                                                                                                                                        Escherichia coli protein sequence SEQ ID NO:469.
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                                                                                                                                                                                                                           AAG98421 standard; Protein; 477 AA
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100.0%;
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Length 477

Best Local Similarity

Query Match

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240
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                                                                                                                                                                                                QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT 300
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                                                 ASEGANARI, VGLTGIDDAARAL, SKSLADVNVKCDFVSVPTHPTITKI, RVLSRNQOLIRLD 120
IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNI1KKIQQDKKG 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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26-MAY-2000; 2000US-207727P-
23-COT-2000; 2000US-242578P-
27-NOV-2000; 2000US-257855P-
22-DEC-2000; 2000US-257931P-
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Xu HH;
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N-PSDB; AAS56025.
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Yamamoto RT,
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                                          The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antiblotics, the essential genes themselves and the discovery of novel antiblotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebslella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The pneumonion is also useful for the identification of potential new targets for antiblotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

Sesential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ASLGANARLYGLTGIDDAARALSKTLAEVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
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antibiotics, comprise sequences of antisense nucleic acids
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93.5%; Pred. No. 1.7e-196;
ive 19; Mismatches 12;
                      Example 3; Seq ID No 13759; 511pp; English.
                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                        477 AA;
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                                                                                                                                                                                                                                                                                                         Seguence
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Matches
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential compared to the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella compendante, Pseudomonas aeruginosa and Enterococcus facealis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to invention used in proliferation, to express these proteins. The proteins and to obtain antibodies capable of binding to the expressed proteins. The antisense nucleic acid sequence is also useful to screen compounds in rational drug discovery comparammes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Con the printed specification, but was obtained in electronic cof the printed specification, but was obtained in electronic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.4%; Score 1350.5; DB 22 57.9%; Pred. No. 1.3e-113; ive 70; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen KL, Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Seq ID No 12079; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                  2000US-191078P.
2000US-206848P.
2000US-242578P.
2000US-24352F.
2000US-253625P.
2000US-26308P.
                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001WO-US09180
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Matches 274; Conservative
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                                                                                                      Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-611495/70.
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                                                                                                                                                               WO200170955-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                         21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-2000;
26-MAY-2000;
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us-09-912-020-325.rag

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The invention relates to a peptide (I) encoded by an operon (II) of Neisseria meningitidis including virulence genes, or a related molecule having a 40% sequence similarity at the peptide or nucleotide level in a Gram-negative bacterium, or its functional fragment, for therapeutic or medicament for treating or preventing a condition (e.g., meningitis) associated with infection by Neisseria or Gram-negative bacteria. The product is useful for veterinary treatment and in a screening assay for the identification of an antimicrobial drug. The vaccines have prophylactic applications. AMU72911-AAU73014 represent N. meningitidis virulence proteins of the invention.
                                                                                                                                                419
               360
                                                                           300
                                                                                                                  361 ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide encoded by operon including virulence genes of Neisseria meningitidis, useful as vaccine component for treating or preventing meningitis and for identifying antimicrobial drug
241 OPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT
                                                                                                                                     STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
                                                                                                                                                                                                                                                                                                                                                                                                        Meningitis; virulence; gene; antibacterial; vaccine; veterinary; infection; Gram-negative bacteria; antimicrobial.
                                                                                                                                                                                              IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQ 473
                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis virulence protein #26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 112-113; 423pp; English.
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                                                                                                                                                                                                                                                                                 AAU72936 standard; Protein; 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2001; 2001WO-GB02003.
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                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MICR-) MICROSCIENCE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis.
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The present sequence is a Helicobacter pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypetide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ONF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify sequences predicted from various ONF were analysed for sequences for vaccine development, the amino acid sequences predicted from various ONF were analysed for significant homology to other known or exported membrane proteins. Having identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
                              74 GLLSVTGNDEAADALDALMVQDGVASYLMRDKQIATTVKLRVVARNQQLIRLDFEEHPNR 133
                                                                                307
                                                                                                                                                                                                             VDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTDFERYR 187
                                                                                                                           GATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAPL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide(s) - useful for vaccines to treat or prevent H. pylori
infection, and to detect Helicobacter
                                                                                                                                                                                         HMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPIE
RLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori nucleic acid sequences and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. pylori cytoplasmic protein, 07ap11409orf4.
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95US-0487032.
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                                                                                                                                                                                                                                                       308 LENAVRGRA 316
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313 LTKALSGOS 321
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AAW20763
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Length 323; Indels

DB 23;

31.2%; Score 745.5; DB 23; 50.5%; Pred. No. 5.1e-59; ive 49; Mismatches 103;

156; Conservative

Matches

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Similarity

Query Match

8 FERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANA 67

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(REGC ) UNIV CALIFORNIA
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RRI 486
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ID AAU3
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and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                 161
                                                                                                                                                                                       51 GGAANVAMNIASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSV-PTHPTITKLRV 109
                                                                                                                                                                                                                                                       EEACFFANAAAGVVVGKLGTSTVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGE 340
                                                                                                                                                                                                                                                                                             341 KVVMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVL 400
                                                                             Gaps
                                                                                                                3 GGAANVANNLTSLKAKVFLCGVVGDDLKGKHFISTLNSIRIDTSGVLIDKTRCTTLKTRI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLM gene cluster; bleomycin gene cluster; polyketide metabolite;
bleomycin; bleomycin analogue; holo-carrier protein; thiazolidine;
thiazoline; bithiazoline; microbial metabolite; sugar.
                                                                                                                                                 63 IAQQQUVRVDKEI----KDPLNADLRKNLLDFIAEKIQEIDGVILSDYNKGVLDFELTQ
                                                                                                                                                                                                                            110 LSRNQQLIRLDFEEGFEGVDP-----QPLHERINQALSSIGALVLSDYAKGAL--ASVQ
                                                                                                                                                                             162 OMIQLARKAGVPVLIDPKGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIA
                                                                                                                                                                                                                  D-YELSALLVTRSEQCMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSL
                                                                                                                                                                                                                                                                   25;
                                                          Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by the bleomycin (BLM) gene cluster ORF30.
                                                        30.7%; Score 734.5; DB 18; Length 40.9%; Pred. No. 7.6e-58; ive 77; Mismatches 154; Indels
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05-FEB-1999; 99US-0118848.
05-JAN-2000; 2000US-0477962.
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                                                        Query Match
Best Local Similarity 40.99
Matches 177; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    408 GYSTSAIIEKIKR 420
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                                       424 AA;
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                                       Seguence
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AABO7556-78 represent proteins encoded by open reading frames (ORFS) 8 to 30 of the BLM (Bleomycin) gene cluster. The proteins encoded by the gene cluster are useful for producing peptides and/or polyketide metabolites, especially bleomycin to bleomycin analogues. They are also useful for chemically modifying biological molecules to produce branched methyl groups, and for coupling amino acids and fatty acids. They may be reacted with an abo-carrier protein and coenzyme A to produce a holo-carrier protein. The BLM gene cluster or catalytic changes can be used individually or collectively to produce thiazolidine, thiazoline, bithiazolime and bithiazoline-containing microbial metabolites. The BLM gene cluster may also be used to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 QP-----LHERINQALSSIGALVLSDYAKGALASVQQMIQLA--RKAGVPVLI--DP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309 AAGTAVATPGTSTWHADELRRLLGG---TGKVCRTGTLPARLLDPAARDR--RVVFTNGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VVSFEEDTPORLIAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNII 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLVGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249 I.DADGSLIFERDRPPVRTFARGSRAPVTAAVGAGDAFTAALTLALAAGADSAVAAELASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPARFTALR-ASAVKPNHAEALRLLDAGEPPPGPARA-DWAAALGDRLLRLTGAERVALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 KGTDFERYRGATLLTPNLSEF-----EAVVGKCKTEEEIVERGMKLIADYELSALLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSEQGMSLLQPGKAPLHMPTQAQE--VYDVTGAGDTVIGVLAATLAAGNSLEEACFFANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGVVVGKLGTSTVSPIELENAVRGRADTGFGVMTEE-ELKLAVAAARKRGEKVVMTNGV
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                                                                                                                                                                  nts useful for peptide and/or bleomycin, production and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.5%; Score 610.5; DB 21; Length 498; 37.7%; Pred. No. 1.7e-46; ive 68; Mismatches 196; Indels 37;
                                                                                                                                                                      New bleomycin gene cluster components useful for
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   Edwards
                                                                                                                                                                                                            polyketide metabolites, especially bleomyc
chemically modifying biological molecules
                                                                                                                                                                                                                                                                                                            Disclosure; Page 97-137; 162pp; English.
Chen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU36261 standard; Protein; 308 AA.
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Best Local Similarity 37.7
Matches 182; Conservative
Sanchez
                                                                   2000-465974/40.
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                                                                                                      N-PSDB; AAA58471.
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the assential genes themselves and the discovery of novel antibiotics, the assential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneunoniae, Pseudomonnas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an eventual prokaryotic cellular proliferation protein.
                                                                                                                                          234 EQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGV 293
                                                                                                                                                                    113 GGNGHLSPAVLARHEHLLEQ-----AQVVVCQLESPLETVGHVLRRAHALGKTVILNPAP 167
                                                                                        Carr GJ;
                                                            --KGTDFERFRGATLLTPNLSEFEAVVGKCKTEEEIVE---RGMKLIADYELSALLVTRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ō
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interococcus faecalis cellular proliferation protein #586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Seq ID No 10892; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                            294 VVGKLGTSTVSPI -- ELENAVRGRA 316
                                                                                                                                                                                                                                                    AAU35299 standard; Protein; 305
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2000US-253625P.
2000US-257931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterococcus faecalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAS53158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAY-2000;
26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 GANARLVGLTGIDDAARALSKSLADVNVKCDFVS-VPTHPTITKLRVLSRNQQLIRLDFE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 EGFEGVDPQPL--HERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDP-- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 RAGVMVVGDVMLDRYWYGPT----SRISPEAPVPVVKVNTIEERPGG-AANVAMNIASL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trawick JD,
                                                                             Pseudomonas aeruginosa cellular proliferation protein #251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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26.5%; Pred. No. 2.5e-09;
Live 50; Mismatches 153; Indels
                                                                                                                  Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Seq ID No 11854; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind JW,
                                                                                                                                                                                                                                                                                                                                                                       2000US-206848P.
2000US-207727P.
2000US-242578P.
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2000US-257931P.
2001US-269308P.
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                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohlsen KL,
Xu HH;
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                                                                                                                                                                                     Seudomonas aeruginosa.
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N-PSDB; AAS54120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 AA;
                                                                                                                                                                                                                          WO200170955-A2.
                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
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Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                    21-MAR-2000;
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                                      14-FEB-2002
                                                                                                                                                                                                                                                                 27-SEP-2001
AAU36261;
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31-MAY-2002
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                                                                                  Sequence
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                                                                                                    Query Match
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                                                                                                                                                                                           166
                                                                                                                                                                                                                                                         ----KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSE 234
                                                                                  Gaps
                                                                                                  13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGG---AANVAMNIASLGANARL 69
                                                                                                                                                      60 IGAVGNDGAGAMMTDLMSQDEINL------TGVTTLEKTATGQAFIMVDNAGENSI
                                                                                                                                                                                    VTIIGSINLD-----TTLRVK-EMPKPGETIHAIEHFTAGGGKGANQAVAAKRSGAETYF
                                                                                                                                     70 VGLTGIDDAARALSKSLA--DVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD-----
                                                                                                                                                                        --FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDP
                                                                                                                                                                                                                       QGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAG-NSLEEACFFANAAAGV
                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleotide sequences isolated from Pyrococcus abyssi encode proteins useful in industry -
                                                                Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Hyperthermophilic archaeon; hyperthermophilic protein.
                                                  Score 191.5; DB &L.,
                                                              DB 22;
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                                                                       22.8%; Pred. No. 7.8e
                                                                                                                                                                                                                                                                                                                                                                                                    Putative P. abyssi cytidylyltransferase #2.
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(IFRE-) IFREMER INST FR RECH EXPL MER.
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Weissenbach
                                                                                                                                                                                                                                                                                   294 VVGKLGTSTVSPIELE 309
                                                                                                                                                                                                                                                                                                    286 TVQRFGAQPSIPYQHE 301
                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-126236/14.
                                                                        Best Local Similarity
Matches 72; Conserv
                                             305 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Pyrococcus abyssi
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Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                   29-OCT-2001
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                                              Seguence
                                                                Query Match
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a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abysas protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up 110 degrees centigrade.

Note: This patent is in the same patent family as WO200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75902 and AAG66436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seduences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 VMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : || || : || : || : || : || : |
IRYVDDVVIGEPGEISLELIKKIKPDVIALGPD-QDFDCRTLKEKLRSIGLKVEVIRLPY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LEAVDWVVSFEE-DTPQRLIAGILPDLLVKGGDYKPEE1AGSKEVWANGG---EVLVLNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                             Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; SEQ ID NO 245; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                      7.9%; Score 189.5; DB 22;
39.9%; Pred. No. 4e-09;
iive 21; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB91034 standard; Protein; 379 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herbicidally active polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---EDGCSTTNIIKKIQQ 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                || |: |||:| :
LYKEDRAKTSKIIKRITE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
nes 55; Conserv
                                                                                                                                                                                                                                                                                                                        148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200210210-A2.
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP33191;
                                                                                                                                                                            Sequence
                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                     165
                                                                                                                                                                                                                                                                                                                                       199
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                              ABP33191
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                                                                                                                                                                                                                                                                                                                    Db
                                  11;
                                                             118 RLDFEEGFEGVD----PQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVP 173
                                                                                                                                                                                           230 VTRSEQGMSLLQPGKAPLHMP-TQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFAN 288
                                                                                                                                                                                                      GANARLVGLTGIDDAARALSKSLAD--VNVKCDFV-SVPTHPT---ITKLRVLSRNQQLI 117
                                                                                                      119 MYPTYFVGRLGEDAHGKLIAEALGDDGCGVHLDYVRSVNNEPTGHAVVMLQSDGQNSIII 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr GJ:
                                  Gaps
                                                                                                                                    -----VGGANMKAWPEIMSDDDLEIVRNAGIVLLQREIPDSINI--QVAKAVKKAGVP
                                                                                                                                                                   --GGAANVAMNIASL
                                                                                                                                                        174 VLIDPKGTDF----ERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALL
                                  49;
                  Length 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae cellular proliferation protein #83.
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                 DB 23;
                7.6%; Score 181.5; DB 23; 25.6%; Pred. No. 8.6e-08; Live 45; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zyskind JW, Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Seq ID No 11035; 511pp; English
                                                  28 PTSRISPEAPVPVVKVNT-----IEERP-
                                                                                                                                                                                                                                                                                           AAU35442 standard; Protein; 306 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-CCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257931P.
16-FEB-2001; 2001US-269308P.
                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-2001; 2001WO-US09180
                                                                                                                                                                                                                              289 AAAGVVVGKLGTSTVSP 305
                                                                                                                                                                                                                                               350 AAASLCVQVKGAIPSMP 366
                                                                                                                                                                                                                                                                                                                              (first entry)
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELITRA PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-611495/70.
N-PSDB; AAS53301.
                         Similarity
379
                                                                                                                                                                                                                                                                                                                                                                                                           WO200170955-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haselbeck R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'amamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2000;
                                                                                                                                                                                                                                                                                                                              14-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2001
                                  81:
                                                                                                                                                                                                                                                                                                            AAU35442;
Sequence
                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-)
                                                                                                                                                                                                                                                                          RESULT 13
AAU35442
                                  Matches
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella preumoniae, Pseudomonas aeruginosa and Enterocccus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; memoduation; haematopolesis regulation; cell differentiation; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; wasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antidiabetic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 GGAANVAMNIASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------ERYRGATLLTPNLSE 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAPLHMPTQAQEVYD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 AEILTGVEVADEQSAVKAASVFHDKGIETVMITLGAKGVFVSRKGKSRIIKGFCVQAI-D 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40 GKGANQAVAAARLGAKVAFISCIGSDSIGKTMKNAFAQEGID-----TTH-----IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 SRNQQLIRLDFEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 VTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPIELE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.4%; Score 178; DB 22; 22.7%; Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 1.3e-45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human ORF2164 protein, SEQ ID NO:4328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-2002
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Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.

Escherichia coli. W0200170955-A2

coli cellular proliferation protein #394.

14-FEB-2002 (first entry)

AAU34813 standard; Protein; 309 AA.

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AAU34813
                                                                            designated ORF (open reading frame) 1-4534, and sequences ABM75054-
ABM75087 represent CDNAs encoding them. The invention also encompasses
polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
referred to as ORFX) proteins, polynucleotides at least 85% identical to
the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
polynucleotides, the recombinant production of ORFX proteins, antibodies
specific for ORFX proteins, methods of detecting ORFX polynucleotides and
polypeptides, methods of screening for modulators of ORFX expression or
activity, and methods of screening individuals for a predisposition to an
ORFX-associated disorder. The ORFX proteins of the invention have a wide
range of biological activities, such as cytokine, cell proliferation,
cell differentiation, immune modulation, haematopoiesis regulation,
tissue growth, angiogenesis, activin tinhibin activity,
chemokinetic activity, haemostatic activity, thrombolytic activity,
receptor/ligand, antiinflammatory activity, thrombolytic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and antiinfective activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, nucleic acids and antibodies may be used in the treatment of cancers, other proliferative disorders such as psoriasis and benign tumours, neurological disorders such as epilepsy and Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORRY nucleic acids may also be used as a source of primers and probes, in the detection of ORRY genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORRY nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORRX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases.
                                                                                                                                                                                                                                                                                                                                                                             Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences ABP31028-ABP35561 represent 4534 novel human proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Page 1338; 2508pp; English.
                                                                                              24-MAY-2001; 2001WO-US17076
                                                                                                                                                24-MAY-2000; 2000US-206690P
                                                                                                                                                                                                                                                 Shimkets RA;
                                                                                                                                                                                                  CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                 2002-106200/14
                                                                                                                                                                                                                                                                                                   WPI; 2002-106200/.
N-PSDB; ABN77217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ransplantation
WO200190366-A2.
                                                 29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis,
                                                                                                                                                                                                                                                    Leach MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Carr GJ;

Trawick JD,

Ohlsen KL, Zyskind JW, Wall D, Xu HH;

2000US-242578P. 2000US-253625P. 2000US-257931P.

2001US-269308P

16-FEB-2001;

27-NOV-2000; 22-DEC-2000;

23-OCT-2000; 23-MAY-2000 26-MAY-2000

(ELIT-) ELITRA PHARM INC

Haselbeck R,

Yamamoto RT,

21-MAR-2001; 2001WO-US09180

27-SEP-2001

21-MAR-2000;

New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids

WPI; 2001-611495/70. N-PSDB; AAS52672.

Example 3; Seg ID No 10406; 511pp; English.

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programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.
                            prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 ARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLKVLSRNQQLIRLDFEEGFE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 ERAGVMVV-GDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGG-AANVAMNIASLGAN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 QNAGSLVVLGSINADHI----LNLQSFPTPGETVTGNHYQVAFGGKGANQAVAAGRSGAN 57
The invention relates to antisense inhibitors of genes essential to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 8.7e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.1%; Score 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 24.5%
Watches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
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Best Local Similarity
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32;

Matches

438

g ò 61

RESULT 15

6

36;

58 IAFIACTGDDSIGESVRQQLATDNIDITPVSVIKGESTGVALIFVNG-E 105		106 GENVIGIHAGANAALSPALVEAQRERIANASALLMQLESPLESVWAAAKIAHQNKTIV 163	LIDPKGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVT 231	164 ALNPAPARELPDELLALVDIITPNETEAEKLTGIRVENDEDAAKAAQVLHEKGIRTVLIT 223	232 RSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAA 291	224 LGSRGVWASVNGEGQ-RVPGFRVQAVDTIAAGDTFNGALITALLEEKPLPEAIRFAHAAA 282	292 GVVVGKLGTSTVSP 305
IAFIACTGDDSIGE	GVDPQPLHERINGA	GENVIGIHAGANAA	LIDPKGTDFER	ALNPAPARELPDEL	RSEQGMSLLQPGKA	LGSRGVWASVNGEG	GVVVGKLCTSTVSP
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Search completed: November 24, 2002, 23:15:49 Job time : 84 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                    OM protein - protein search, using sw model
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November 24, 2002, 23:13:04 ; Search time 51 Seconds (without alignments) 899.140 Million cell updates/sec Run on:

US-09-912-020-325 2393 1 MKVTLPEFERAGVMVVGDVM......FEDGCSTINIIKKIQQDKKG 477 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	ADP-heptose syntha			ADP-heptose syntha				rfaE protein [impo	ADP-	probable adp-d-qly	kinase [imported]	ADP-heptose syntha	ADP-heptose syntha		probable bifunctio	ADP-heptose syntha	glycerol-3-phospha	aut protein NMB207	probable transfera	aut protein - Alca	fructokinase BH185	ribokinase PA1950		probable sugar kin		ribokinase [import	ribokinase (EC 2.7	ribokinase [import	probable carbohydr
SUMMARIES	QI	20.	G91120	F85965	AG0891	AI0080	C64127	A83022	F87700	н81319	C71887	G84936	B64627	H81154	н81951	T34841	H70350	H70317	C81009	G82031	I39548	A83882	B83403	E72311	AH0947	A75041	AB2029	D69690	B87367	AC0942
	Length DB	:		477 2							463 2			323 2						168 2								293 1		
ф	Query Match L	100.0	99.7	7.66	94.7	86.8	71.5	56.4	37.8	36.1	34.2	33.9	33.8	31.5	31.2	24.8	23.6	16.4	14.6	14.2	13.0	8.4	•	8.1	8.0	7.9	7.9	7.7	7.7	7.7
	Score	2393	2385	2385	2265	2076	1712	1350.5	904.5	863	819.5	811	809.5	753.5	745.5	594	564.5	391.5	348.5	340.5	311.5	201.5	197	194	192.5	189.5	188	184.5	₹.	183.5
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ALIGNMENTS

	RESULT 1	
	ADD-hent	BOSOLOS BOSOLOS BOSOLOS GUNTHAGO HOMOLOG - DECHONICHIA COLI (etrain K-12)
	N; Altern	ກຸຊ
	C;Specie	C;Species: Escherichla coli
	C;Date:	C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002 C:Accession: R65093
	R;Blattn	S.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
	.A.; ROS	.A.; Rose, D.J.; Mau, B.; Shao, Y.
	Science	2277, 1453-1462, 1997
	A;Title:	A/FILLE: The Complete genome sequence or Escherichia coli K-iz. A-Daference umbar: A64730, MITH-07426617. DMIN-0726613.
	A; Access	A; Accession: B65093
	A; Status	A;Status: preliminary; nucleic acid sequence not shown; translation not shown
	A; Molecu	A: Molecule type: Day
	A: Cross-	AKBSIGUES: I-4/1 KELAID AKTORS-TREFERENCES: GRARDONART: GREDONOGE: NID-G1789431: PIDN:AAC7608R.1: PID:G17894
	A; Experi	A; Experimental source: strain K-12, substrain MG1655
	c; superi	amily: nypotnetical protein badaz
	Query	Query Match 100.0%; Score 2393; DB 1; Length 477;
	Matche	$\overline{}$
	ΟŶ	1 MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI 60
	qq	1 MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI 60
	Oy 6	61 ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
	9 qa	61 ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
	Qy 121	
	Db 121	1 FEGGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 180
	Qy 181	
	Db 181	1 TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL 240
	Qy 241	1 OPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT 300
	Db 241	
	Qy 301	STVSPIELENAVRGRADTGFGVWTEEELKLAVAAARKRGEKVVWTNGVFDILHAGHVSYL 360
	Db 301	
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ADP-heptose synthase (EC 2.7.-.) [imported] - Salmonella enterica subsp. enterica servar Typhi
ADP-heptose salmonella enterica subsp. enterica servar Typhi
A) Note: this species has also been called Salmonella typhi
C; Bate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C; Accession: AG0891
R; Parklill, J; Dougan, G; James, K.D; Thomson, N.R; Pickard, D; Wain, J; Church
th, T; Connerton, P; Cronin, A; Davis, P; Davies, R.M.; Dowd, L.; White, N.; Farr
S; Moule, S; O'Gaora, P.
Nature 413, 484-812, 2001
A; Authors: Parry, C; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A; Reference number: AB0502; PMID:11677608
A; Reference number: AB0502; PMID:11677608
A; Residues: 1-477 < < PAR>
A; Cross-references: GB:AL513382; PIDN:CAD07725.1; PID:g16504277; GSPDB:GN00176
C; Genetics:
A; Genetics:
C; Genetics:
C; Superfamily: hypothetical protein b3052
C; Keywords: phosphotransferase
A;Reference number: A85480; MUID:21074935;.PMID:11206551
A;Accession: F85965
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-477 <STO>
A;Cross-references: GB:AE005174; NID:g12517628; PIDN:AAG58186.1; GSPDB:GN00145; UWGP:A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: Z4405
C;Superfamily: hypothetical protein b3052.
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Pred, No. 3:6e-144;
1; Mismatches 1;
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Best Local Similarity 99.6%;
Matches 475; Conservative
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Accession: F85965
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
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Pred. No. 3.6e-144;
1; Mismatches 1;
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Best Local Similarity 99.6%;
Matches 475; Conservative
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ADP-Deptose synthase homolog - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1995 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
C;Accession: C64127
R;Fielschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weddman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Accession: C64127
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: C64127
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-76 <TICR>
A;Cross-references: GB:U3228; GB:L42023; NID:g1574362; PIDN:AAC23172.1; PID:g1574367
C;Superfamily: hypothetical protein b3052
                                                                                                                                                                STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360
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                                   241 QLGKPPLHLPTQAKEVFDVTGAGDTVIGVLAAALAAGNSLEESCFLANAAAGVVVGKLGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
71.5%; Score 1/12, C.
Best Local Similarity 71.0%; Pred: No. 2.2e
Matches 331; Conservative 58; Mismatches
                                                181
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C; Species: Yersinia pestis
C; Species: Versinia pestis
C; Species: Versinia pestis
C; Accession: A10080
A; Prentice, M.B.
A; Printle: A2: 527, 2001
A; Stelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A; Reference number: AB0001; MUID:21470413; PMID:11586360
A; Recession: A10080
A; Accession: A10080
A; Residues: 1-476 < KUR>
A; Residues: 1-476 < KUR>
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                                                               STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
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                Indels
 1.5e-136;
ches 12;
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llarity 86.1%; Pred. No. 1.6e-124;
Conservative 32; Mismatches 34;
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                19; Mismatches
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probable ADP-heptose synthase Cj1150c [imporfed] - Campylobacter jejuni (strain NCTC C; Species: Campylobacter jejuni
C; Species: Campylobacter jejuni
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C; Accession: H81319
C; W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; Churcher, C.; Basham, D.; Chill C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A; Reference number: A81250; MUID:20150912; PMID:10688204
A; Accession: H81319
A; Accession: H81319
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-461 cPAR>
A; Rosidues: 1-461 cPAR>
A; Rosidues: 1-461 cPAR>
A; Cross-references: GB:AL139077; GB:AL11168; NID:g6968444; PIDN:CAB73404.1; PID:g696
C; Genetics:
            Venter, J.C.; Fraser,
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fra Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87700
A;Accession: F87700
A;Residues: Preliminary
A;Molecule type: DNA
A;Residues: 1-483 <STO>
A;Cross-references: GB:AE005673; NID:q13425394; PIDN:AAK25602.1; GSPDB:GN00148
C;Genetics:
A;Genetics:
C;Superfamily: hypothetical protein b3052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 GANARLVGLTGIDDAARALSKSL-ADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFE 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 37.8%; Score 904.5; DB 2; Best Local Similarity 45.1%; Pred. No. 5e-50; Matches 214; Conservative 66; Mismatches 186;
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Pred. No. 2e-47;
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C, Superfamily: hypothetical protein b3052
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43.1%;
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C;Species: Caulobacter crescentus
C;Date: 2O-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: F87700
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
                                                                                                                                                                                                                                                                                                                                                                                 P.; Hickey, M.J.; Br
A.; Larbig, K.; Lim,
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A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                          LPS biosynthesis protein RfaE PA4996 [imported] - Pseudomonas aeruginosa (strain PA01)
                                                                                                                                                                                                                                                                                                                                       C; Accession: A83022
R; Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic RA; Reference number: A83022
A; Reference number: A8302
A; Reference town per a proportunistic RA; Reference number: A83022
A; Reference number: A8302
A; 
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                                                                                                                                                                                                                                                                                    C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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C;Superfamily: hypothetical protein b3052
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Matches 274; Conservative
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C;Species: Buchnera sp.
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
C;Stacession: G849Watenabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp A; Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: G84936
A;Reference type: DNA
A;Molecule type: DNA
A;Residues: 1-315 <£TO>
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                                                                                                                                                                                                        303 VSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYLAN 362
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                                                                                                                                 AS---LEEIALILNQTHPKILPLEKL---LETLERNQQKIVFTNGCFDILHKGHASYLQK
                                  :| |:|:|| :| | | :| SKYSHASLITPNRAELEQALHLKLDSHANLSKALQILQETYHIAMPLVTLSEQGIAFLEK
                                                                                                      GKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTST
                                                                                                                                                                                                                                                                                                          ARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRLIA
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C;Species: Helicobacter pylori
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; Pred. No. 2.4e-44;
63; Mismatches 93;
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A;Experimental source: strain APS
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kinase [imported] - Buchnera sp. (strain APS)
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50.0%;
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Matches 156; Conservative
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C; Species: Helicobacter pylori
A; Vartety: strain J99
C; Date: 12-Feb-1999
C; Date: 12-Feb-1999
C; Accession: C71887
C; Accession: C7188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 TGIDDAARALSKSLADVNVKCDFVSV-PTHPTITKLRVLSRNQQLIRLDFEEGFEGVDP- 130
                                                                                                                                                                                      129 DPQPLHERINQALSSIGALVLSDYAKGALAS--VQQMIQLARKAGVPVLIDPKGTDFERY 186
                                                                                                                                                                                                                                                                                     123 LENELIALFDEKIKDFKAVVLSDYAKGVLTPKVCKAVIEKAKVLNIPVLVDPKGSDFNKY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --IAPAKALEVYDVTGAGDSVIAVLAFCLANEIEIFKACELANEAAAVVSKIGSVSVSF 300
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                                                                                                                                                      LVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEGV 128
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     Gaps
                                                                            13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLVGL 72
                                                    ERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANAR 68
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  20;
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PDILVKGADYKDKLVVGADIV----SRVELIDFEEGFSTSKIIEKI-KDKK 461
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90; Mismatches 158; Indels
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Matches 193; Conservative
  Conservative
203;
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Best Local Similarity
Matches 159; Conserv
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Gene: rfaE; NMA1034
A; Gene: NMB0825
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A;Cross-references: GB:AE002435; GB:AE002098; NID:g7226049; PIDN:AAF41238.1; PID:g722606
A;Experimental source: serogroup B, strain MC58
C;Genetics:
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                      C. Accession: B64627
R. Tomb, J. F., White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
R. Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
R. Tomb, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujli, C.; Bowman, C.; Watthey, L.
Mature 388, 539-547, 1997
A. Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A. Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A. Reference number: A64520; MUID: 97394467; PMID: 9252185
A. Accession: B64627
A. Status; preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: LNA A;Molecule type: LNA A;Molecule type: Local type: 1-461 CTOMA A;CTOSS-references: CB:AE000596; GB:AE000511; NID:g2313982; PIDN:AAD07904.1; PID:g2313999 C;Superfamily: hypothetical protein b3052
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Datession: Hall54
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
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  Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLVGL 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                  27;
                                                                                                                                                                                                                                                                                                                                                                                 Length 461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQ 473
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                 33.8%; Score 809.5; DB 1;
40.6%; Pred. No. 5.1e-44;
rative 88; Mismatches 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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A; Status: preliminary
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Matches 191;
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Cispecies: Neisseria meningitidis
Cispecies: Neisseria meningitidis
Cispecies: Neisseria meningitidis
Cispecies: Obervay-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
Cispecies: Obervay-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
Cispecies: Obervay-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
Riparkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
A; Jature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
A; Recence number: A81775; MUD:2022556; PMID:10761919
A; Accession: H81951
A; Accession: H81951
A; Residues: 1-323 APAR>
A; Residues: 1-323 APAR>
A; Residues: 1-323 APAR>
A; Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84303.1; PID:g737
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;; Pred. No. 3.7e-40;
49; Mismatches 103;
                                              49; Mismatches 100;
  DB 2;
Score 753.5; DB 2 Pred. No. 1.1e-40;
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50.5%;
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Best Local Similarity 50.5%
Matches 156; Conservative
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C;Keywords: phosphotransferase
                                                Conservative.
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probable bifunctional synthase /transferase - Streptomyces coelicolor C:Species: Streptomyces coelicolor C:Accession: T34841
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Roliver, K.; Harris, Data Library, February 1999
A:Reference number: Z21559
A:Reference number: Z21559
A:Reference number: Z21559
A:Reference number: Z21559
A:Residues: preliminary; translated from GB/EMBL/DDBJ
A:Residues: 1-463 < Coll>
A:Residues: 1-463 < Coll>
A:Residues: 1-463 < Coll>
A:Cross references: EMBL:AL035478; PIDN:CAB36595.1; GSPDB:GN00070; SCOEDB:SC2G5.08
A:Cross references: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC2G5.08
C:Superfamily: hypothetical protein b3052
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Best Local Similarity 36.3%; Pred. No. 2.6e-30;
Matches 173; Conservative 71; Mismatches 189; Indels 44; Gaps
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us-09-912-020-325.rsp

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 24, 2002, 22:30:34 Run on:

.; Search time 38 Seconds (without alignments) 520.637 Million cell updates/sec

US-09-912-020-325 2393 1 MKVTLPEFERAGVMVVGDVM......FEDGCSTINIIKKIQQDKKG 477 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		di			SUMMARIES			
Result		Query						
No.	Score	Match	Length	BO	. QI	Δ	Description	;
1	2393	100.0	477	н	RFAE_ECOLI	Ω.	P76658 escherichia	ia
6	1712	7	476	-	RFAE_HAEIN	0	005074 haemophilus	S T
m	819.5	m	463	Н	RFAE_HELPJ	ď	Q9zkz0 helicobacte	te te
4	811	33.	315	Н	Y060_BUCAI	Δ.	8 buchnera	ap
Ŋ	809.5	m	461	Н	RFAE_HELPY	0	025529 helicobacte	e.
9	184.5	7.7	293	Н	RBSK_BACSU	д	bacillus	sn
7	178	7.4	306	Н	RBSK_HAEIN	Δ,		ns
œ	176	7.4	294	-	RBSK_BACHD	a	bacillus	ha
σ	169	7.1	309		RBSK_ECOLI	Δ,	P05054 escherichia	ja
10	166.5	7.0	298	-	YIHV_ECOLI	Δ.	_	ja
11	164.5	6.9	320	-	YDJE_BACSU	0	bacillus	ns
12	158	9.9	309	7	K6P2_ECOLI	Δ.		ja
13	153	6.4	307	-	SCRK_VIBAL	Δ,	P22824 vibrio algi	gi
14	153	6.4	322	-	RBSK_HUMAN	a		eu
15	152.5	6.4	307	-	SCRK_SALTY	<u>.</u>		æ
16	151.5	6.3	148	-	YD36_METJA	a	58732 methanococc	S
17	150.5	6.3	318	-	RBSK_SCHPO	0		сh
18	150	6.3	129	Н	TAGD_BACSU	Δ,	P27623 bacillus su	sn
19	145.5		307	-	SCRK_ECOLI	Δ,	P40713 escherichia	ja
20	142	5.9	307	Н	SCRK_KLEPN		P26420 klebsiella	æ
21	141	•	316	Н	K1PF_RHOCA	Δ.		er
22	135.5		544	~	CH60_NEIGO .	Δ,		9
23	133	•	370	-	CTPT_PLAFK	Δ.	~	E
24	132.5		544	-	CH60_NEIMB	Δ,	P42385 neisseria m	E
22	131		313	-	YEIC_ECOLI	Δ.	_	ja
56	130.5		300	-	RBSK_LACLA		O9cf42 lactococcus	ns
27	130.5		315		YDJH_ECOLI	<u>а.</u>	77493 escherichia	ţa
28	130.5		544		CH60_NEIFL	Δ.	-	44
59	129.5	5.4	313	٦	K1PF_HAEIN	Δ.	P44330 haemophilus	ns.
30	129.5	5.4	544	Н	CH60_NEIMA	Δ.		E
31	128	5.3	319	Н	SCRK_SOLTU	Д		å
32	125.5	5.2	1182	-	DP3A_RICPR	0	005974 rickettsia	æ
33	122.5	5.1	324	-	YM02_MYCTU	a	Q10391 mycobacteri	ij

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P33020 escherichia O33013 mycobacteri Q49396 mycoplasma Q942c4 rattus norv P25332 saccharomyc P33060 saccharomyc Q99447 homo sapien P49583 caenorhabdi Q6460 rattus norv P55263 homo sapien O9x5v3 rhizobium l O88022 streptomyce
YEII_ECOLI SR54_MYCLE CTBU_MYCGE CTBU_MAT RBSK_YEAST MX3_YEAST PX3_LHUAN CTPT_CAEL ADK_RAT ADK
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ALIGNMENTS

RESULT 1 RFAE_ECOLI DE RFAE_ECOLI STANDARD; PRT; 477 AA.	15-JUL-1999 (Rel. 38,	15-JUL-1999 (Rel. 38, 15-JUN-2002 (Rel. 41,	3 ADP-heptose synthase (EC 2.7). N REAR OR WAAR OR B3052.			Scherichia. K NCBI TaxiD=562;				A Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., A Rilev M. Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F.,			The complete genome sequence of Escherichia coli K·12.";				This SWISS-PROT entry is copyright. It is produced through a collaboration		use by non-profit institutions as long as its content is in no	modified and this statement is not removed. Usage by and for commerc	entities requires a license agreement (See http://www.isb-sib.ch/announce/			R HSSP; P27623; 1COZ.		InterPro;	InterPro; IPR002173;	Pfam; PFO(_	R PROSITE; PS00583; PFKB_KINASES_1; 1. R DROSITE: DS00584: DFKR KINASES 2: PALSE NES		SEQUENCE 477 AA; 51050 MW; 0F03CBE160B95389 CKC64;	<pre>Best Local Similarity 100.0%; Pred: No. 1.6e-135; Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>
RE CI	P E	D L	D E	os	88	38	R.S.	RP C	RX	RA RA	R.	RA	RT	Α ς Έ	ខ	ပ္ပ	ဗ	ع د	ខ	ပ္ပ	88	3 8	38	DR	DR DR	DR	DR	D C	D. S.	E E	3	SS	-

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InterPro; IPR004820; Cytidylyltransf
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                                                                                                                                                                                                                                    STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360
ASLGANARLVGLTGIDDAARALSKSLADVNVKCDEVSVPTHPTITKLRVLSRNQQLIRLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.
McKenney K., Sutton G., Fitzhugh W., Fleids C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Ulterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,

    -i- PATHWAY: Lipopolysaccharide core biosynthesis.
    -i- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.

                                                                                                                                                                                                                                                                                                                                                121 FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG
                                                                                                                   TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL
                                                                                                                                                                            QPGKAPLHMPTQAQEVYDVTGAGDTV1GVLAATLAAGNSLEEACFFANAAAGVVVGKLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ADP-heptose synthase (EC 2.7.-.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR004821; Cyt_tran_rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U32828; AAC23172.1; -. HSSP; P27623; ICO2.
TIGR; HI1526; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RFAE OR WAAE OR HI1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter J.C.;
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O05074;
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61
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366
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    -1- PATHWAY: Lipopolysaccharide core biosynthesis.
    -1- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.

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OSIXED.

OSIXED.

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2002 (Rel. 41, Last annotation update)

15-UNN-2002 (Rel. 41, Last annotation update)

ADP-heptose synthase (EC 2.7...).

ADP-heptose synthase (EC 2.7...).

Helicobacter pylori J99 (Campylobacter pylori J99).

Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 EFERAGYMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGAN
                                                                                                                                                                                                                                                                                         67 ARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 LHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTDFERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFREDTPQRLIAGILP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINES-99120557; PubMed-9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis 'Trust T.J.;
                                                                                                                          Complete proteome
                                                                                                                                                                                                                            ;
                                                                                                                                                                                      Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQ 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427 DLLVKGGDYKPEEIAGSKEVWANGGDVKVLNFENGCSTINVIEKIK 472
                                                                                                                                                                               71.5%; Score 1712; DB 1; ilarity 71.0%; Pred. No. 5.2e-95; Conservative 58; Mismatches 77:
                                                                                                                        Lipopolysaccharide biosynthesis; Transferase; Co
SEQUENCE 476 AA; 51945 MW; 4F241C08D2C6951E
            Pfam; PF00294; pFkB; 1.
Pfam; PF01467; Cytidylyltransf; 1.
TIGRRAMS; TIGR00125; Cyt.Tran_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; FALSE_NEG.
PROSITE; PS00584; PFKB_KINASES_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic sequence comparison of
IPR002173; PfkB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                         Similarity
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Matches 331;
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InterPro;
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NCBI_TaxID=210;
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025529;
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                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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            SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                    73 TGIDDAARALSKSLADVNVKCDFVSV-PTHPTITKLRVLSRNQQLIRLDFEEGFEGVDP- 130
                                                                                                                                                                                                                                                                                                                                                                                   64 VGDDLEGKHFISTLKTRGIDTSGVLIDKTRCTTLKTRIIAQNQQIVRVDKEI----KDPL 119
                                                                                                                                                                                                                                                                                                                                                                                                                      183
                                                                                                                                                                                                                                                                                                                                                                                                                                242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 VSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYLAN 362
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                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                    72
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4 ILVIGDLIADYYLWGKSERLSPEAPVPVLEVKKESKNLGGAANVANNLTSLKAKVFLCGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKYSHASLITPNRAELEQALHLKLDSHANLSKALQILQETYHIAMPLVTLSEQGIAFLEK
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                                                                                                                                                                                                                                                                                                                    VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLVGL
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                                                                                                                            InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR00213; PfkB.
InterPro; IPR00213; PfkB.
Pfam; PF00294; pfkB; I.
Pfam; PF00467; Cytidylyltransf; 1.
IIGRFAMS; TIGR00125; Cyt_tran_rel; 1.
PROSTTE; PS00584; PFKB_KINASES_1; FALSE_NEG.
PROSTTE; PS00584; PFKB_KINASES_1; FALSE_NEG.
Lipopolysaccharide blosynthesis; Transferase; Complete proteome. SEQUENCE 463 AA; 50926 MW; 770367403E771124 CRC64;
                                                                                                                                                                                                                                                                     DB 1; Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423 GILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIKKIQQ 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=118099;
                                                                                                                                                                                                                                                                    34.2%; Score 819.5; DB 1;
41.0%; Pred. No. 6.5e-42;
ive 87; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical sugar kinase BU060.
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                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 193; Conserv
                                                                                                                     1002
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P57168;
15-JUN-2002 (
                                                                                                                                                                                                                                                                     Query Match
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MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fletschmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                            Buchnera sp. APS.";
Nature 407:81-86(2000).
-!- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                        H.;
aphids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 QKEKKPIHFPAASKIASDVTGAGDTVIAIIAASLATGYSLEEACFYANIGASIVIQKKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKVTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteome
                                                                                     , Sakaki Y., Ishikawa
bacterial symbiont of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interpro; IPR002173; PfkB.
Pfam; PF00294; pfkB; 1.
PROSITE; PS00583; PFKB.KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; FALSE_NEG.
HYDOTHETical protein; Transferase; Kinase; Compl.
SEQUENCE 315 AA; 35023 WW; 6983707C601EFD25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.9%; Score 811; DB 1;
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
ADP-heptose synthase (EC 2.7...-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 1.3e
63; Mismatches
SEQUENCE FROM N.A.
STRAIN-TOKYO 1998;
MEDLINE-20445173; Pubmed-10993077;
Shigenobu S., Watanabe H., Hattori M.,
"Genome sequence of the endocellular be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP001118; BAB12783.1; -.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLVGL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S., Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams N.D., Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M. Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                  -i- PATHWAY: Lipopolysaccharide core biosynthesis.
                                                                                                                                      "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |: :: || |:||||||||||||| | :|
240 GEL-VNCPTIAKEVYDVTGAGDTVIASLTLSLLESMSLKDACEFANAAAAVVVGKMGSAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 GKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIGHTAMS: TIGRO0125; CYLLIAD_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; FALSE_NEG.
PROSITE; PS00584; PFKB_KINASES_2; FALSE_NEG.
Lipopolyaeccharide biosynthesis; Transferase; Complete SEQUENCE 461 AA; 50688 MW; FE6A42A5301C16A5; CRC64;
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es_165;
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40.6%; Pred. No. 2.6e
tive 88; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR004821; Cyt_tran_rel.
InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR002173; PfkB.
Pfam; PF00294; pfkB; 1.
Pfam; PF01467; Cytidylyltransf; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE000596; AAD07904.1; -.
                                                                                                                                                                         Nature 388:539-547(1997).
-!- PATHWAY: Lipopolysacc
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                                                                                                                      Venter J.C.;
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G. Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Murita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Rubel C., Medique C.,
RA Kobayashi Y., Koetter P., Kohingstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Robyashi F., Koetter P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Rodina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Yossarotti A.,
RA Takeuchi M., Tamakoshi A., Tangai T., Takhashi H., Takemaru K.,
RA Vasti A., Wambutt R., Wedler H., Weitzenegger T.,
RA Vasti A., Wambutt R., Wedler E., Wastenegger T.,
RA Winters P., Wibbat A., Tamamoco H., Vamane K., Vasumoto K., Yata K.,
RA Winters P., Wibbat A., Tamamoco of the Gram-positive bacterium Bacillus
R. T., Franklan R., Parklein E., Yoshikawa H., Danchin A.;
R. The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Presecan E., Moszer I., Boursier L., Cruz Ramos H.C., De La Fuente V., Hullo M.-F., Lebnog C., Schleich S., Sekowska A., Scnq B.H., Villani G., Kunst F., Danchin A., Glaser P., "The Bacillus subtilis genome from gerBC (311 degrees) to lick (334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
-!- CATALYTIC ACTIVITY: ATP + D-ribose = ADP + D-ribose 5-phosphate.
-!- PATHWAY: Ribose metabolism; first step.
-!- SUBCELLULAR LOCATION: CYtoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: OT OTHE PPKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                               Woodson K., Devine K.M.; "Analysis of a ribose transport operon from Bacillus subtilis."; Microbiology 140:1829-1838(1994).
                                                                                                                                                                                     Firmicutes; Bacillales; Bacillaceae; Bacillus.
                   P36945; P96733;
01-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
1-JUN-2002 (Rel. 41, Last annotation update)
Ribokinase (EC 2.7.1.15).
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  293
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  STANDARD;
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                                                                                                                                                               Bacillus subtilis,
                                                                                                                                                                                                              NCBI_TaxID=1423;
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RBSK_BACSU
                                                                                                                                                                                          Bacteria;
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RBSK_BACHD
Q9K6K1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGG-AANVAMNIASLGANARLVG 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 293;
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                          RNEVEELLS -> DKK (IN REF. 1).
DCB69533E53253EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 184.5; DB 1; Length 25.3%; Pred. No. 0.00023; .
Live 41; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 AA.

..., WOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ribokinase (EC 2.7.1.15).
Hagmont.
                                                                                                                                                                                                                                                                                                                                                  Transferase, Kinase, Complete proteome. CONFLICT 284 293 TRNEVEELLS
                        or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                    Pfam; PF00294; pfkB; 1.
PRINTS; PR00990; RIBOXINASE.
PROSITE; PS00583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                         EMBL; 225798; CAA81049.1; -.
EMBL; 292953; CAB07465.1; -.
EMBL; 299122; CAB15609.1; -.
PIR; 542711; S42711.
HSSP; P05054; IRKD.
Subfilist; B610877; rbsK.
InterPro; IPR002173; PfKB.
InterPro; IPR002173; Ribokinase.
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STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
                                                                                                                                                                                                                                                                                                                                                                                                293 AA; 31138 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 25.3% tes 80; Conservative
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P44331;
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Matches
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"Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GGAANVAMNIASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 SRNQQLIRLDFEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMI---- 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 FEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAPLJIMPTQAQEVYD 258
                                                                                               -:- CATALYTIC ACTIVITY: ATP + D-ribose - ADP + D-ribose 5-phosphate.
-:- PATHWAY: Ribose metabolism; first step.
-:- SUBCELLULAR LOCATION: CYCOOJASSMIC (By similarity).
-:- SIMILARITY: BELONG TO THE PFKB FAMILY OF CARROHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 AEILTGVEVADEQSAVKAASVFHDKGIETVMITLGAKGVFVSRKGKSRIIKGFCVQAI-D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Kinase; Complete proteome.
SEQUENCE 306 AA; 32204 MW; 3DCE8810827C8E84 CRC64;
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SEQUENCE FROM N.A.
SERAIN-C-125 / JCM 9153;
MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasak∴ R.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.4%; Score 178; DB 1; 22.7%; Pred. No. 0.00059;
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Last annotation update)
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45; Mismatches
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PRINTS, PR00990; RIBOKINASE.
PROSTIE; PS00583; PFRB_KIRASES_1; 1.
PROSITE; PS00584; PFRB_KINASES_2; 1.
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InterPro; IPR002139; Ribokinase.
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15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U32732; AAC22163.1; -. HSSP; P05054; 1RKD.
                                                                  Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66; Conservative
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STRAIN=K12
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  between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                           70 VGLTGIDDAARALSKSLADVNVKCDFVSVPTHPT--ITKLRVLSRNQQLI------R 118
                                                                                                                                                                                                                                                                                                                                                                                      119 LDFEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDP 178
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             ----KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 QGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVV 294
        halodurans and genomic sequence comparison with Bacillus subtilis.", Nucleic Acids Res. 28:4317-433(2000).
-- CATALYTIC ACTIVITY: ATP + D-TIDOSE = ADP + D-TIDOSE 5-phosphate.
--- PATHWAX: Ribose metabolism; first step.
--- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
--- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                         13 VMVVGDVMLDRYWYGPTSRISPEAPV--PVVKVNTIEERPGG-AANVAMNIASLGANARL 69
                                                                                                                                                                                                                                                                                                                            6 ITVVGSINMDMV-----TITDVVPVQGETVLGKDFRTVPGGKGANQAVAAARLGANVRM 59
                                                                                                                                                                                                                                                                                                                                                                                                        120 PDYVAAFE-----QELAASDVVLLQ--LEIPLETVAYVLEFCAKHHVTTVLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
"Complete genome sequence of the alkaliphilic bacterium Bacillus
                                                                                                                                                        Length 294;
                                                                                                                                                                                                                                                                                     49; Mismatches 132; Indels
                                                                                                                                                                                                                                                                 7.4%; Score 176; DB 1; 25.4%; Pred. No. 0.00074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Last annotation update) Ribokinase (EC 2.7.1.15). RBSK OR B3752 OR Z5253 OR ECS4694.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                     80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VOSFGAQGGMPTKAQ 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                            Local Similarity
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SEQUENCE FROM N.A.
STRAIN=K12;
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P05054;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Ruhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-91179935; PubMed-9519409; Sigrell J.A., Cameron A.D., Jones T.A., Mowbray S.L.: Sigrell J.A., Cameron A.D., Jones T.A., Mowbray S.L.: "Structure of Escherichia coli ribokinase in complex with ribose and dinucleotide determined to 1.8-A resolution: insights into a new structure 6:183-193(1998).
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-93315143; PubMed-7686882;
MEDLINE-93315143; Plunkett G. III, Daniels D.L., Blattner F.R.;
"DNA sequence and analysis of 136 kilobases of the Escherichia coli genome: organizational symmetry around the origin of replication.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
MEDLINE=86224052; PubMed=3011794;
Hope J.N., Bell A.W., Hermodson M.A., Groarke J.M.;
*Ribokinase from Escherichia coli K12. Nucleotide sequence and
overexpression of the rbsK gene and purification of ribokinase.";
J. Biol. Chem. 261:7663-7668(1986).
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MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Acotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signell J.A., Cameron A.D., Mowbray S.L.;
"Induced fit on sugar binding activates ribokinase.";
J. Mol. Biol. 290:1009-1018(1999).
-- CATALYTIC ACTIVITY: ATP + D-ribose - ADP + D-ribose
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MEDLINE-99370056; PubMed=10438599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
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MEDLINE=98046763; PubMed=9385653;
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STRAIN=168;
MEDLINE=98044033; PubMed=9384377;
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SEQUENCE FROM N.A.
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034768;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         67 ARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFE 126
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                                                                                                                                                                                                                                                                                                                                                                                                                            175 LIDP---KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVT 231
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                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                    9 ERAGVMVV-GDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGG-AANVAMNIASLGAN 66
                                                                                                                                                                                                                                                                                                          2 QNAGSLVVLGSINADHI----LNLQSFPTPGETVTGNHYQVAFGGKGANQAVAAGRSGAN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93347969; PubMed=8346018; Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.; Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.; Fanalysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes."; Nucleic Acids Res. 21:3391-3398(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                       Length 309;
                                                                                                                                                                                                                                    / Match 7.1%; Score 169; DB 1; Length 305
Local Similarity 24.5%; Pred. No. 0.002;
les 77; Conservative 47; Mismatches 154; Indels
                                                                                                                                                                PRINTS; PR00990; RIBOKINASE.
PROSITE; PS00583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
Transferase; Kinase; 3D-structure; Complete proteome.
SEQUENCE 309 AA; 32290 MW; 75372984fb64060E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1993 (Rel. 27, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical sugar kinase yihv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 AA
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                                                                                          PDB; IRKA; 20-MAR-00.
PDB; IRKS; 31-AUG-99.
EcoGene; EG10818; rbsK.
InterPro; IPR002173; PfkB.
InterPro; IPR002193; Ribokinase.
Pfam; PF00294; pfkB; 1.
                       AE000452; AAC76775.1; -. AE005607; AAG58955.1; -. AP002566; BAB38117.1; -.
M13169; AAA51476.1;
L10328; AAA62105.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 GVVVGKLGTSTVSP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 AIAVTRKGAQPSVP 296
                                                          PIR; A26305; KIECRB.
PDB; 1RKD; 04-MAR-98.
PDB; 1RK2; 07-JUN-00
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STRAIN=K12 / MG1655;
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P32143;
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              EMBL;
                                   EMBL;
EMBL;
                         EMBL;
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MEDLINE=98116660; PubMed=9455482;
Kasahara Y., Nakai S., Ogasawara N., Yata K., Sadaie Y.;
Kasahara Y. Of the GroESL-CotA region of the Bacillus subtilis genome, containing the restriction/modification system genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 YRGATLLTP-NLSEFEAVVGKCKTEEEIVER--GMKLIADYELSA-----LLVTRSEQ 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLVGL 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                          EMBL; L19201; AAB03016.1; ALT_INIT.

EMBL; AE000464; AAD13445.1; ALT_INIT.

PIR; $40827; $40827.

ECGENE; EG11848; yihv.

PICAFPC; IPR00213; PfkB.

PROSTIE; PS00534; pfkB; 1.

PROSTIE; PS00534; PFKB_KINASES_1; FALSE_NEG.

PROSTIE; PS00534; PFKB_KINASES_2; 1.

PROSTIE; PS00634; PFKB_KINASES_2; Xinase; Complete proteome. SEQUENCE 298 AA; 31727 MW; 24D347B04542909E CRC64;
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Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.0%; Score 166.5; DB 1; Best Local Similarity 26.5%; Pred. No. 0.0028; Matches 79; Conservative 39; Mismatches 135;
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15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical sugar kinase ydjE.
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A Guiseppi G., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
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Wall A., Wambutt R., Wedler E., Wedler H., Weitzeneger F.,
Wither B., Wammanto B., Wammanto K.,
Wallari A., Wambutt R., Wedler E., Wedler H., Weitzeneger F.,
Wither B., Wambutt R., Wedler E., Wedler H., Weitzeneger F.,
Wallari A., Wambutt R., Wedler E., Wedler H., Weitzeneger F.,
Wallari A., Wambutt R., Wedler E., Wedler H., Weitzeneger F.,
Wallari A., Wambutt R., Wedler E., Wedler H., Weitzeneger F.,
Wallari A., Wambutt R., Wedler E., Wedler H., Weitzeneger F.,
Wallari A., Wambutt R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 KVGKDPFGYFLKRTLDAVHVDTSML-VMDEKAPTTLAFVSLKQNGERDFVFNRGADALFT 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 VVCIGELLIDFF-----CTDVDVDLMEGRQFLKSAGGAPANVSAAIAKLGGDAAFSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 RYRGATLLTPNLSEFEAVVGKC-----KTEEEIV-----ERGMKLIADYELSAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.9%; Score 164.5; DB 1; Length 320; 4.5%; Pred. No. 0.004;
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SEQUENCE 320 AA; 34256 MW; A54E095039953B7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Subtilist; BG12796; ydjE.
InterPro; IPR002173; PfkB.
Pfam. PF00294; pfkB.
PROSTIE; PS00583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
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HSSP; Q9TVW2; 1DGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                subtilis.";
Nature 390:249-256(1997).
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K6P2_ECOLI STANDARD; PRT; 309 AA.
P06999; P78065; P78260;
01-APP-1988 (Rel. 07, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
6-phosphofructokinase isozyme 2 (EC 2.7.1.11) (Phosphofructokinase-2).
PFRB OR B1723.
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Escherichia coli and the nature of a mutation, pfkBi, causing a high
level of the enzyme.";
J. Mol. Biol. 168:265-305(1983).
-!- CATALYTIC ACTIVITY: ATP + D-fructose 6-phosphate " ADP + D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- MISCELLANEOUS: ONLY 10% OF THE ACTIVITY PRESENT IN THE WILD-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fructose 1,6-bisphosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97426617; PubMed=9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- SIMILARITY: PHOSPHOFRUCTOKINASE-1 SHOWS NO HOMOLOGY TO PHOSPHOFRUCTOKINASE FOUND IN BLOCHI. ALTHOUGH THE REACTION CATALYSED IS THE SAME, THE TWO ENZYMES HAVE A DIFFERENT EVOLUTIONARY ORIGIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alba H., Baba T., Fullta K., Hayashi K., Inada T., Isono K., Itoh Kasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchii T., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchii T., Ratomoto Y., Horiuchii T., Maka Saquence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN IS PHOSPHOFRUCTOKINASE-2.
-!- MISCELLANEOUS: THIS ENZYME IS NOT TO BE CONFUSED WITH
6-PHOSPHOFRUCTO-2-KINASE (EC 2.7.1.105), WHICH IS ALSO CALLED
                                                                                                                                                                                                                                                                   Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    minor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence of gene pfkB encoding the mphosphofructokinase of Escherichia coli K-12."; Gene 28:337-342(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97251357; PubMed=9097039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=84262485; PubMed=6235149;
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DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHOFRUCTOKINASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1,6-DIPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Daldal F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daldal F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
There are no restrictions on ig as its content is in no
                                                                                                                                                                                                                                                                                                             Transferase; Kinase; Glycolysis; Complete proteome.

CONFLICT 26 38 GARCTAPVFEPG -> ENCAVPHRCSNP (IN REF. 1 AND 4).

CONFLICT 155 171 AAQKQGIRCIVDSSGEA -> LRKNKGSAASSTVLGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 ARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFE---EGFEGVDP---- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----QPLHERINQALSSIGALVLSDYAKGA-LASVQQMIQLARKAGVPVLIDPKGTDFER 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 YRGA-----TLLTPNLSEFEAVVGK------CKTEEEIVERG--MKLIADYELSALL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 VTRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 GVDSENCIQVVPP------PVKSQ---STVGAGDSMVGAMTLKLAENASLEEMVRFGVA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -EHLVSLLADENV------PVATVEAKDWTRQNLHVHVEASGEQYRFVMPGAALN 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSRISPE----APVPVVKVNTIEERPGGAANVAMNIASLGANARLV----GLTGIDDA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio alginolyticus.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 LSAALAIGNIELVKPNQKELSALVNRELTQPDDVRKAAQEIVNSGKAKRVVVSLGPQGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 158; DB 1; Length 309; Pred. No. 0.0092; 37; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               A93BEBE0D5801309 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               (IN REF. 1).
PV -> AL (IN REF. 1).
SM -> RL (IN REF. 1).
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ID SCRK_VIBAL

AC P2824;
DT 01-AUG-1991 (Rel. 19, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DF 01-NOV-1995 (Rel. 32, Last annotation update)

DF 01-Cottokinase (EC 2.7.1.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-91071601; PubMed-2174811;
Blatch G.L., Scholle R.R., Woods D.R.;
European Bioinformatics Institute.
                                                                                                         EMBL; AE000267; AEC74793.1; --
EMBL; D90814; BAA15500.1; ALT_INIT.
EMBL; D90815; BAA15506.1; ALT_INIT.
EMBL; K00128; AAA24320.1; --
PIR; AA4950; KIECPB.
SWISS-2DPAGE; P06999; COLI.
ECOZDBASE; E036.6; GTH EDITION.
                                                                                                                                                                                                                            ECOGENE; EG10700; pfkB.
InterPro; IPR002173; PfkB.
Pfam, PF00294; pfkB. 1.
PROSITE; PS00583; PFKB.KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                               245 246 1 257 258 309 AA; 32456 MW;
                                                                                               EMBL; K02500; AAA24321.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 AGSAATLNQGTRLCS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 AAGVVVGKLGTSTVS 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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CONFLICT
SEQUENCE
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Best Local S
Matches 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence and analysis of the Vibric alyinolyticus sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 LTGIDDAARALSKSLADVNVKCDF-VSVPTHPTITKLRVLSRNQGLIRLDFEEGFEGVDP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 QPLHERINQALS--SIGALVLSDYA-----KGALASVQQMIQLAKKAGVPVLIDPK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 LRD------EVWQDQSEIQAVVMKAVAMADVVKFSEEELLFLTDSTSMAQGLQQIAAM 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 ELSALLVTRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNS---- 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 FMVKPSADQFMSVEDMGNFKQGDWLHVCSISLANEPSRSSTFEAIKRAKAAGGFISFDPN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 VMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGA-ANVAMNIASLGANARLVG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VWVIGDAVVD------LIPESETSLLKC-----PGGAPANVAVAIARLSGKSAFFG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVGDDPFGRFMQSILDQEGVCTEFLIKDPEQRTST------VVVDLDDQGERSFT 97
                                                                                   phosphate.
-i- SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARROHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTDFERYRGATLLTPNLSEFEAVVGKCK-----TEEEI------VERGMKLIADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70;
                                                          -!- CATALYTIC ACTIVITY: ATP + D-fructose = ADP + D-fructose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.4%; Score 153; DB 1; Length 307; Best Local Similarity 23.5%; Pred. No. 0.018; Matches 78; Conservative 53; Mismatches 131; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                             ransferase; Kinase.
SEQUENCE 307 AA; 33045 MW; AF9C96CBB781C6EF CR364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ribokinase (EC 2.7.1.15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wightman P.J.;
Thesis (2000), University of Edinburgh, U.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --LEEACFFANAAAGVVVGKLGTSTVSPIELE 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 PVVSSAIQWANGCGALATTQKGAMTALPTQTE 300
                                                                                                                                                                                                                                                                                                                                                                            Pfan, PF00294; pfkB; 1.
PROSITE; PS00583; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                   EMBL; M76768; AAA27556.1; -.
                                                                                                                                                                                                                                                                                                                    PIR, JQ0782; JQ0782.
HSSP, Q9TVW2; LDGY.
InterPro; IPR002173; PfkB.
                  uptake-encoding region.";
Gene 95:17-23(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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Q9H477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Best Loc
Matches
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                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGAMTSWVCKVGKDSFGNDYIENLKQNDISTEF----TYQTKDAATGTASIIVNNEGQNI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPT-----ITKLRVLSRNQQL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 IRLDFEEGFEGVDPQPLHERINQALSSIG-ALVLSDYAKGALASVQQMIQLARKAGVPVL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----IITLGAEGCVVLSQTEPEPKHIPTEKVKAVDTTGAGDSFVGALAFYLAXYPNLSL 287
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                               ERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERP-----GGAANVAMNIAS 62
                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + D-ribose = ADP + D-ribose 5-phosphate.
                                                  -i- PATHWAY: Ribose metabolism; first step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 IDP----KGTDFERYRGATLLTPNLSEFEAV----VGKCKTEEE----IVERGMKLIADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAADAGEAALVLLKRGCQVV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 ELSALLVTRSEQGMSLL-QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLA--AGNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobactería; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                         54;
                                                                                                                                                                                                                                                                                                                                            ; Score 153; DB 1; Length 322;
; Pred. No. 0.019;
48; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                      322 AA; 34143 MW; 50D0E7161F33E94B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                 PROSITE; PS00583; PFKB_KINASES_1; FALSE_NEG. PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 EEACFFANAAAGVVVGKLGTSTVSP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 EDMLNRSNFIAAVSVQAAGTQSSYP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
MEDLINE-92236409; PubMed=1809835;
                                                                                                                                                                                                                              InterPro; IPR002173; PfkB.
InterPro; IPR002139; Ribokinase.
Jefam; PF00294; PfkB; I.
PRINTS; PR00990; RIBOKINASE.
                                                                                                                                                                                         EMBL; AJ404857; CAC12877.1; -. EMBL; BC017425; AAH17425.1; -. HSSP; P05054; 1RK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequ
01-AUG-1992 (Rel. 23, Last anno
                                                                                                                                                                                                                                                                                                                                                6.48; 25.58;
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 25.55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fructokinase (EC 2.7.1.4).
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Plasmid pUR400
                                                                                                                                                                                                                                                                                                            Kinase.
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NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                           Transferase;
SEQUENCE 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCRK_SALTY
P26984;
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                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (| : | : | : | : | 11| : | 154 SFDPN------IRPDLMQDQALLLACLDRALHMANVVKLSEEELVFISSSNDLA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 IGAVGGDFFGRYMRHTLQQEQVDVSHMYLDDQHRTSTVVVDLDDQGERTFTFMVRPSADL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLIRLDFEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQOMIQLARKAGVPV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 AKVWVLGDAVVD------LLPESE-----GRLLQCPGGAPANVAVGVARLGGNSGF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 AGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGA-ANVAMNIASLGANARL 69
                                                                                                                                                                                            phosphate.
SIMILARITY: BELONGS TO THE PFKB FAMILY OF CARBOHYDRATE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 LIDPKGIDFERYRGATLITPNLSFFEAVVGKC------KIEEBIV-----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 RGMKLIAD-YELSALLVTRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAAT
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                                                                                                                           MOl. Microbiol. 5:2913-2922(1991).
-!- CATALYTIC ACTIVITY: ATP + D-fructose = ADP + D-fructose 6-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 307;
Aulkemeyer P., Ebner R., Heilenmann G., Jahreis K., Schmid K. Wriedden S., Lengeler J.W.; Molecular analysis of two fructokinases involved in sucrose metabolism of enteric bacteria.";
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37 AA; 32916 MW; E01CB770CE20B329 CRC64;
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23.8%; Pred. No. 0.019;
Live 48; Mismatches 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S16044; S16044.
PIR; S18524; S18524.
HSSP; Q9TWW2; IDGY.
InterPro; IPR002173; PfkB.
PR0SITE; PS00584; PFKB_KINASES_1; 1.
PROSITE; PS00584; PFKB_KINASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; x61005; CAA43323.1; -.
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tes 81; Conserva
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Job time :
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                                                                                                                                      November 24, 2002, 23:11:44 ; Search time 95 Seconds
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                          OM protein - protein search, using sw model
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	(without alignments) 1034.573 Million cell updates/sec
Title: Perfect score:	US-09-912-020-325 2393
Sequence:	1 MKVTLPEFERAGVMVVGDVMFEDGCSTTNIIKKIQQDKKG 477

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

671580 Total number of hits satisfying chosen parameters: 671580 segs, 206047115 residues Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Database :

SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
5: sp_luwertebrate:*
6: sp_mammal:* sp_unclassified:* sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:* sp_rvirus:* sp_bacteriap:* sp_archeap:* sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES .

Description	Q8xbm4 escherichia	174 salmonella	O8xew9 salmonella	fy8 salmonella	9rfy7 salmonella	Q8zi60 yersinia pe	eme6 pasteurell	O9huq9 pseudomonas	3046 haemophilus	09a2c5 caulobacter	Ppne5 campylobac	98154 rhizobium	90x5i8 neisseria m	3k004 neisseria	O91r14 neisseria m
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% Query Match Length DB	477	477	477	477	473	476	476	474	342	483	461	496	313	323	323
% Query Match	99.7	95.1	94.7	94.0	93.0	86.8	71.1	56.4	46.9	37.8	36.1	36.1	31.5	31.5	31.2
Score	2385	2276	2265	2250	2225	2076	1701	1350.5	1122	904.5	863	863	753.5	753.5	745.5
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Q9WWX7 Q9FB11 Q9Z5B5 Q8R6E8 Q66836	QBRF00 O66572 Q51060 Q9JXF0 Q9JWI8	Q8Y2M6 Q43999 Q8RBP6 Q9KBR8 Q9I2F4	091782 08RD45 08R109 09UZ37 08YW32	09459M0 0842W9 0944F4 08U1T9 058466 09SHH5
110	14444			100
307 498 463 323 315	150	346	300 300 300 300 300	315 315 315 315
28.4 24.8 24.8 23.6	17.0 16.4 15.4 14.6	13.1 13.0 9.3 8.4	0.08 0.00 0.00 0.00 0.00 0.00	
678.5 610.5 594 584.5 564.5	407.5 391.5 368.5 348.5 340.5	314 311.5 221.5 201.5 197	192.5 190.5 189.5 188	184.5 183.5 182.5 181.5 181.5 181.5
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ALIGNMENTS

908BM4 PRELIMINARY; PRT; 477 AA. 901-MAR-2002 (TrEMBLrel. 20, Last sequence update) 901-JUN-2002 (TrEMBLrel. 21, Last annotation update) 902-JUN-2002 (TrEMBLrel. 21, Last annotation update) 903-JUN-2002 (TrEMBLrel. 21, Last annotation update) 903-JUN-2002 (TrEMBLrel. 21, Last annotation update) 904-JUN-2002 (TrEMBLrel. 21, Last annotation; Enterobacteria; gamma subdivision; Enterobacteria; gamma subdivision; Enterobacteria; gamma subdivision; Enterobacteria; gamma sequence of enterobaction and annotation and andotation and andotation and annotation and annotation and andotation andotation and andotati

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Best Local Sim
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.
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"ADP-heptose synthase (rfaE) gene of salmonella typhimurium.";
submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF155126; AARZ0933.1; -
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                                                                                  99.7%; Score 2385; DB 16; Length 477; 99.6%; Pred. No. 2.1e<sup>-</sup>142; 1. Indels 0.
                                                      Complete proteome.
E 477 AA; 51064 MW; BB877FEF6636E67C CRC64;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                   TIGREAMS; TIGRO0125; cyt_tran_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
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Pfam; PF0024; pfkm; 1.
TIGRFAMS; TIGH00125; Cyt_tran_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
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InterPro; IPR004820; Cytldylyltransf.
InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR002173; PfkB.
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InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR002173; PfkB.
Pfam; PF01467; Cytidylyltransf; 1.
Pfam; PF00294; pfkB; 1.
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                                                                                                      Conservative
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                                                                                             Similarity
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01-JUN-2001
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01-JUN-2002
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Matches 475;
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D., Wain J.,
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                                                                                                                                                                                                                                                                          61 ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPT1TKLRVLSRNQQLIRLD 120
                                                                                                                                                                                                                                                                                                   FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 180
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Salmonella typhi.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNY-2002 (TrEMBLrel. 21, Last annotation update)
Bifunctional, putative sugar nucleotide transferase domain
ADP-L-91ycero-D-manno-heptose synthase (EC 2.7.-.) (ADP-he
synthase).
RFAE OR STW3200 OR STY3379.
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MEDLINE-21534947; PubMed-11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard
                         51169 MW; 269475F3FF9EB9EF CRC54;
                                                                     Score 2276; DB 2;
Pred. No. 1.6e-135;
); Mismatches 10;
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93.9%;
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477 AA;
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Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis R.M., Dowd L., Whitele, Farrar J., Feltwell T., Hamlin W., Haque A., Hen T.T., Hollroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., And Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Whitehead S., Barrell B.G.; Moule S., O'Gaora P., Parry C., Whitehead S., Barrell B.G.; Rellond J., Stevens K., Whitehead S., Barrell B.G.; Rellond J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome sequence of a multiple drug resistant Salmonella renterica serrowar Typhi CT18."; Nature 413:848-852(2001).

R. Babl., AE008847; AAL22074.1; Babl., AE008847; AAL22074.1; Babl., AE008847; AAL22074.1; Babl., AE008847; Cytidylyltransf.

R. InterPro; IPRO04820; Cytidylyltransf.

R. InterPro; IPRO04820; Cytidylyltransf.

R. InterPro; IPRO04820; Cytidylyltransf.

R. InterPro; IPRO04820; Cytidylyltransf.

R. Pfam: PF00485; Cytidylyltransf.

R. Pfam: PF00485; Cytidylyltransf.

R. TIGRFAMS; TIGR00125; Cyt.tran_rel; 1.

R. Pfam: PF00485; Pfam: Minnses_1; UNKNOWN_1.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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477 AA; 51124 MW; E4FF6BIDEE80568C CRC64;
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Last sequence update)
Last annotation update)
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(TrEMBLrel. 13, I
(TrEMBLrel. 21, I
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Matches 445; Conservative
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NCBI_TaxID=28901;
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01-JUN-2002 (
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"The rfaE gene from Escherichia coli encodes a bifunctional protein involved in the biosynthesis of the lipopolysaccharide core precursor ADP-L-glycero-D-manno-heptose.";
J. Bacteriol. 182:488-497(2000).
EMBL: AFIG5661; AAD49846.1; -.
HSSP; P27623; 1C02.
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Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
Salmonella.
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                                                                                                                                                                                                InterPro; IPR04822; Cytidylyltransf.
InterPro; IPR04821; Cyt_tran_rel.
InterPro; IPR00173; PfkB.
Pfam; PF01467; Cytidylyltransf; 1.
Pfam; PF00294; pfkB; 1.
TIGRFMS; TIGR00125; Cyt_tran_rel; 1.
PROSITE; PG0583; PFKB KINASE_1; UNKNOWN 1.
SEQUENCE 477 AA; 51119 WW; 9215BA18BD655FF7 CkC54;
                     Valvano M.A., Marolda C.L., Bittner M., Glaskin-Clay Klena J.D.;
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Last annotation update)
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MEDLINE=20096694; PubMed=10629197;
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MEDLINE=20096694; PubMed=10629197;
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Best Local Similarity 92.99
Matches 442; Ccnservative
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Raker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., A Faltulter S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., A Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., A Feltwell T., Hamilin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; T. "Genome sequence of Yersinia pestis, the causative agent of plague."; Muture 413:523-527(2001).

E MBL: AJ41444; CAC89508.1; -.

InterPro; IPR004821; Cyt_tran_rel.

InterPro; IPR064831; Cyt_tran_rel.

InterPro; IPR064831; Cyt_tran_rel.

InterPro; IPR064831; Cyt_tran_rel.

InterPro; IPR064831; Cyt_tran_rel.
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella.
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Last annotation update)
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STRAIN-PM70;
MEDLINE-21145866; PubMed=11248100;
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Valvano M.A., Marolda C.L., Bittuet m., creaming the Klena J.D.;
Klena J.D.;
"The rfaE gene from Escherichia coll encodes a bifunctional protein "The rfaE gene from Figure 1 incomplysaccharide core precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ASLGANARLYGLTGIDDAARALSKTLAEVNVKCDEVSVPTHPTITKLRVLSRNQQLIRLD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
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STAIN-CO-92 / BIOVAR ORIENTALIS;
MEDILINE-214-0413; PubMed-11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ADP-heptose synthase (EC 2.7.-.).
RFAE OR PPO0654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.0%; Score 2225; DB 2; 92.2%; Pred. No. 2.6e-132; ive 20; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01467; Cytidylyltransf; 1.
Pfam; PF00294; pfkB; 1.
TIGRRAMs; TIGR00125; Cyt_tran_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
VARJANT 236 236 E > G.
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                                                                                                                                                                                                                                                               InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR002173; PfkB.
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                                                                                              involved in the blosynthesis of the ADP-L-glycerc-D-manno-heptose."; J. Bacteriol. 182:488-497(2000).
EMBL; AF163662; AAD49847.1; -.
HSSP; P27623; 1COZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 AA; 50868 MW;
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, Saier M.H., Hancock R.E.W., Lory S., Olson M.V. genome sequence of Pseudomonas aeruginosa PAO1,
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                                              opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004912; AAG08381.1;
HSSP; P27623; 1C02.
                                                                                                                                                                                                                                                                                                                                                                                         274; Conservative
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01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
ADP-heptose synthase.
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    Reizer J.,
"Complete g
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Q48046;
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Matches
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STRAIN-ATC. 15692, PAO1;
MEDLINE-20437337; PubMed-10984043;
Stover C. K., Pham X.-Orr., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Colitry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Bridky L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 ARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQOLIRLDFEEGFE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 GVDPQPLHERINQALSSIGALVLSDYAKGALASVQOMIQLARKAGVPVLIDPKGTDFERY 186
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                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                       7 EFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGAN 66
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                                                                                                                                                                                                                                                                                                 Query Match 71.1%; Score 1701; DB 16; Length 476; Best Local Similarity 69.7%; Pred. No. 2.9e-99; Matches 327; Conservative 65; Mismatches 77; Indels 0
      T.S., Ka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          476 AA; 51884 MW; C4137ECC7B2F02D1 CRC64;
May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001). EMBL; AE006127; AAK02968.1; HSSP; P27623; ICOZ.
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01-MAR-2001 (TIEMBLrel. 16, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
LPS blosynthesis protein RfaE.
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Pfam; PF00294; pfkB; 1.
TIGRFAMs; TIGR00125; cyt_tran_rel; 1.
                                                                                                       InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR004821; Cyt_tran_rel.,
InterPro; IPR002173; PfkB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG 180
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MKLSMPREDQAPVLVVGDVMLDRYWHGATSRISPEAPVPVVRVEQHEDRPGGAANVALNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 QPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT
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MEDLINE-96070820; PubMed-7592970;
Lee N., Sunshine M.G., Engstrom J.J., Gibson B.W., Apicella M.A.;
Netation of the htrB locus of Haemophilus influenzae nontypeable
strain 2019 is associated with modification of lipid A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.4%; Score 1350.5; DB 16; Length 474; 57.9%; Pred. No. 3.7e-77; ive 70; Mismatches 128; Indels 1;
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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Last annotation update)
                                                                                                                                                                                    InterPro; IPR004820; Cytidylyltransf.
InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR02173; PfkB.
Pfam; PF00467; Cytidylyltransf; 1.
TIGRPAMS; TIGR00125; Cyt_tran_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
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                                                    MEDLINE=95172727; PubMed=7868252;
Lee N.G., Sunshine M.G., Apicella M.A.;
"Molecular cloning and characterization of the nontypeable Haemophilus
influenzae 2019 rfaE gene required for lipopolysaccharide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN—ATCC 19089 / CB15;
STRAIN—ATCC 19089 / CB15;
MISTRAIN—21173698; PubMed=11259647;
Mistrain W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Bisen J., Heidelberg J.E., Alley M.R.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Crawn M.B., Khouri H., Shetty J., Berry K.,
Utterback T., Trant K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
"Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                          247 LHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPI 306
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                                                                                                                                                                                  46.9%; Score 1122; DB 2; Length 3 67.2%; Pred. No. 5.8e-63; Live 47; Mismatches 59; Indels
                                                                                                                                                             37538 MW; 4FFB55031E3927C8 CRC64;
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Last annotation update)
phosphorylation of the lipooligosaccharide.";
J. Biol. Chem. 270:27151-27159(1995).
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01-JUN-2001 (TrEMBLrel. 17, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                            Infect. Immun. 63:818-824(1995).
Infect. Immun. 63:818-824(1995).
EMBL: U17642: AAC43516.1; -.
Interpro: IPR002173; PfkB.
Pfam: PF00294; pfkB: 1.
SEQUENCE 342 AA; 37538 MW; 41
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217; Conserv
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NCBI_TaxID=155892;
                               SEQUENCE FROM N.A.
                                                                                                      biosynthesis.";
                                                                                                                                                                                    Query Match
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123 EGFEGVDPQPLHERINQALSSIGALVLSDYAKGAL--ASVQQMIQLARKAGVPVLIDPKG 180
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STRAIN-NCTC 1168;
MEDLINE-20150912; PubMed-10688204;
MEDLINE-20150912; PubMed-10688204;
MEDLINE-20150912; PubMed-10688204;
Barkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Ouail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
The genome sequence of the food-borne pathogen Campylobacter jejuni
nature 403:665-668(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
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                                                                                                                                                                                                                                                 483 AA; 49621 MW; 9CD4ED6CD784608A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 21, Last annotation update)
Putative ADP-heptose synthase.
WAAE OR CJ1150C.
                                                                                                                                               TIGREAMS; TIGRO0125; cyt_tran_rel; 1.
PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
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InterPro; IPR004820; Cytidylyltransf.
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                            InterPro; IPR004821; Cyt_tran_rel.
InterPro; IPR002173; PfkB.
Pfam; PF01467; Cytidylltransf; 1.
Pfam; PF00294; pfkB; 1.
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Matches 214; Conservative
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Query Match
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123 LENELIALFDEKIKDFKAVVLSDYAKGVLTPKVCKAVIEKAKVLNIPVLVDPKGSDFNKY 182
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                               461 AA; 51237 MW; 490D9FDB4EB58322 CRC64;
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                             Query Match 36.1%; Score 863; DB 16; Best Local Similarity 43.1%; Pred. No. 2e-46; Matches 203; Conservative 90; Mismatches 158;
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TIGRFAMs; TIGR00125; cyt_tran_rel; 1.
EMBL, AL139077; CAB73404.1; -- HSSP; P27623; ACOZ. InterPro: IPR004820; Cytidylyltransf. InterPro: IPR004821; Cyt_tran_rel. InterPro: IPR002413; PfkB. Pfam: PF00467; Cytidylyltransf; 1. Pfam; PF00294; pfkB; 1.
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STRAIN-MAFF303099;
MEDLINE-21082930; Pubmed-11214968;
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01-JUN-2002
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O98I54;
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SEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAG 292
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                                                                                                                                                                                                                                                                                                                                                                                                                        124 GFEGVDPQ?LHE-----RINQALSSIGALVLSDYAKGALAS--VQQMIQLARKAGVP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 VLIDPKGTDFERYRGATLLTPNLSEFEAVVGKCK-TEEEIVERGMKLIADYELSALLVTR 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 SEKGMSVVGPDEA-RHIATQAREVFDVSGAGDTVIATFALALASGADPVAAASIANAAGG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 VSFEEDTPQRLIAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNFEDGCSTTNIIK 469
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                             LPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 VVVGKLGTSTVSPIELENAV-RGRADTGF--GVMTEEELKLAVAAARKRGEKVVMTNGVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWV
                                                                                                                                                                                                                                  22;
                                                                                                                                                                                              Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-NMB;
Kahler C.M., Stephens D.S.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125564; AAD32179.1; -.
InterPro: IPR002173; PfkB.
Pfam; PF00294; pfkB; 1.
PROSTE: PS00583; PFKB.KINASES_1; UNKNOWN_1.
                                                                                                                                                        496 AA; 51449 MW; 49DB1E271653AA76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 12, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                            tch 36.1%; Score 863; DB 16; al Similarity 43.3%; Pred. No. 2.2e-46; 209; Conservative 69; Mismatches 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative ADP-heptose synthetase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313
EMBL, AP003000; BAB49662.1; -. InterPro; IPR004820; Cytidylyltransf. InterPro; IPR004821; Cyt_tran_rel. InterPro; IPR002173; PfkB. Pfam: PF01467; Cytidylyltransf; 1. Pfam: PF01467; Cytidylyltransf; 1. TIGRFAMS; TIGR00125; Cyt_tran_rel; 1.
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                                                                                                                                      Complete proteome. SEQUENCE 496 AA;
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01-NOV-1999
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RLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEG 127
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Matches 156;
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STRAIN=MCSB / SEROGROUP B;
STRAIN=MCSB / SEROGROUP B;
Tettelin H., Saunder=10710307;
Tettelin H., Saunder=10. Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Oin H., Vamathevan J., Smith H.O., Fraser C.M., Maxon B.R., Rappuoli R., Venter J.C.; Smith H.O., Fraser C.M., Maxon B.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                              243 YQPTRAQEVYDVSGAGDTVIAGMGLGLAAGÇTMPEAMYLANTAAGVVVAKLGTAVCSFAE 302
                                                                                                                                                                                                                                  GATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAPL 247
                                                                                                                                                                                                                                                                                 248 HMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPIE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=491;
                                                       Gaps
                                                                                                                              68 RLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEG 127
                                                                                                                                                                              128 VDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTDFERYR 187
                                                                                          8 FERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 FERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 FAQAKVLVVGDVMLDRYWFGDVSRISPEAPVPVAKIGRIDQRAGGAANVARNIASLGGRA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 323;
                           DB 2; Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49; Mismatches 100; Indels
                                                    Indels
E940F9CC3786EA15 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
                        31.5%; Score 753.5; DB 2;
51.5%; Pred. No. 8.8e-40;
iive 49; Mismatches 100;
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51.5%; Pred. No. 9.2e-40;
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PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                       323 AA.
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  33833 MW;
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TIGR; NMB0825; -.
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                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Best Local Similarity
  313 AA;
                                      Local Similarity
nes 159; Conserv
                                                                                                                                                                                                                                                                                                                                  308 LENAVRGRA 316
                                                                                                                                                                                                                                                                                                                                                         303 LIKALSGQS 311
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01-DEC-2001
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  SEOUENCE
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                           Query Match
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Q9K004
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STRAIN=Z2491 / SEROGROUP A / SEROTYPE 4A;
MEDLINE=20187481; PubMed=10722605;
Klee S.R., Nassif X., Kusecek B., Merker P., Beretti J.L., Achtman M.,
GATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAPL 247
                                                                                                                                                                                                                                                                                                                                         248 HMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPIE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis (serogroup A), and
Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 FERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANA 67
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MEDIANE-2022556; PubMed-10761919;
MEDIANE-2022556; PubMed-10761919;
MEDIANE-2022556; PubMed-10761919;
MEDIANE-10. Achiman M., James K.D., Bentley S.D., Churcher C.,
Riee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd & Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,
Rajandream M.A., Rutherford K.M., Slmmonds M., Skelton J.,
Whitehead S., Spratt B.G., Barrell B.G.,
"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                                                                                                                                     VDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKGTDFERYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09.07.7.
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative DP-heptose synthetase (EC 2.7.) (Putative ADP-heptose-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;; Complete proteome.
323 AA; 35124 MW; 044C34579F719370 CRC64;
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PROSITE; PS00583; PFKB_KINASES_1; UNKNOWN_1
Transferase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 LENAVRGRA 316
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68 RLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEG 127
14 FAQAKVLVVGDVMLDRYWFGDVSRISPEAPVPVAKIGRIDQRAGGAANVARNIASLGGKV 73
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	133	
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_	ATTV	
	VASYLMRDKQI	
	ALMVQDG	
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Search completed: November 24, 2002, 23:18:30 Job time: 98 secs

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^{1 |: |::} 313 LTKALSGQS 321

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November 24, 2002, 23:14:19; Search time 37 Seconds (without alignments) 379.317 Million cell updates/sec
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2393
1 MKVTLPEFERAGVMVVGDVM......FEDGCSTTNIIKKIQQDKKG 477
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                262574 seqs, 29422922 residues
                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                     Title:
Perfect score:
Sequence:
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                                                                                                                       Run on:
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Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ion	e 4521, Ap			2, App	10,	4	281	8	7	9	ω,	7	~	S	390	2,	33,	9	34,	7,7	7	7	7	7,	'n	35,	V
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	achamas
SUMMAKIES	ID	US-09-134-001C-4521	US-09-134-001C-5560	US-09-134-001C-5583	US-08-826-611-2	US-08-804-227C-10	US-08-804-198-4	US-09-199-637A-281	US-08-479-614-8	US-08-479-614-2	US-08-826-611-6	US-08-955-957A-3	US-08-961-539-2	US-09-185-826-2	US-08-479-614-5	US-09-134-001C-3900	US-09-320-878-2	US-09-105-537-33	US-09-105-537-6	US-09-091-097-34	US-08-461-722-2	US-08-336-251-2	PCT-US94-06362-2	US-09-428-517-2	US-08-627-873-7	US-08-116-098-2	US-08-687-590-32	115-08-790-912-4
	DB	4	4	4	m	7	7	4	~	7	ო	4	7	4	~	4	٣	4	4	4	₹	4	Ŋ	4	7	ч	4	c
	Length DB	315	137	312	347	3724	3724	859	362	361	328	366	303	303	345	321	3739	3739	11877	507	547	547	547	4150	1056	552	552	1861
d	Query Match	6.9	6.3	5.7	5.7	9.9	5.6	5.4	4.9	4.9	4.8	4.8	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.5	4.4	4.4	4.4	4.3	4.3	4.3	4.3	۶ ۲
	Score	165.5	150	137.5	137.5	134.5	134.5	130	117.5	116.5	116	115.5	112.5	112.5	111.5	110	110	110	110	107.5	106	106	106	104	103.5	102.5	102.5	102
	Result No.	1	7	m	4	5	φ	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

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Sequence 12, Appl Sequence 12, Appl	Sequence 2, Appli	Sequence 3, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 5, Appli	J.	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 450, App	Sequence 454, App	Sequence 12, Appl	Sequence 6, Appli	Sequence 4, Appli	Sequence 4, Appli	
US-09-222-817-12 US-09-222-786-12	US-09-144-085-2	US-08-804-227C-3	US-09-144-085-1	US-09-335-409-5	US-09-568-102-5	US-09-567-969-5	US-09-568;480-5	US-09-568-486-5	US-09-568-472-5	US-09-567-899-5	US-09-071-035-450	US-09-071-035-454	US-08-804-227C-12	US-08-804-198-6	US-07-642-734C-4	US-08-439-009A-4	
w 4	4	7	4	m	4	4	4	4	4	4	4	4	7	7	7	m	
530 530	6095	1864	5087	7257	7257	7257	7257	7257	7257	7257	1313	1313	1891	1891	3567	3567	
4.4.	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	4.2	
101.5 101.5	101	100	100	100	100	100	100	100	100	100	99.5	99.5	99.5	99.5	99.5	99.2	
28	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT. US-09-11 US-09-11 FORTH FILE FILE CURN FILE CURN PRION PRI	RESULT 1 US-09-134-001C-4521 US-09-134-001C-4521 Sequence 45.21. Application US/09134001C Patent No. 6380370 GENERAL INFORMATION: APPLICANT: LYON DOUGETE-Stamm et al APPLICANT: LYON DOUGETE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCCC; TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS TORRENT APPLICATION NUMBER: US/09/134,001C CURRENT APPLICATION NUMBER: US 60/064,964 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR PILING DATE: 1997-11-08 PRIOR FILING DATE: 1997-08-14 SEQ ID NO 4521 LENGTH: 315 LENGTH: 315 TYPE: PRT TYPE: PRT TYPE: PRT CORANISM: Staphylococcus epidermidis
Query Best Matche	Query Match 6.9%; Score 165.5; DB 4; Length 315; Best Local Similarity 22.6%; Pred. No. 3.1e-08; Matches 77; Conservative 56; Mismatches 142; Indels 65; Gaps 13;
Qy Dp	2 KUTLPEFERAGVMVVGDVMLDRYWYGPTSRISPEAPVPVKVNTIEERPGGAANVAMN 59 : : : : : :
Qy	60 IASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRL 119
Qy 1: Db	120 DFEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQ 161
Qy 10	162 QMIQLARKAGVPVLIDPKGTDFERYRGATLLTPNLSEFEAVVGKCKTEE 210 :: : ::
Qy 2: Db 2:	211 EIVERGMKLIADYELSALLVTRSEGGMSLLQPGKAPLHMPTQAQEVXDVTGAGDTVIGVL 270 11
Qy 2.	271 AATLAAG-NSLEEACFFANAAAGVVVGKLGTSTVSPIELE 309

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153 IAQITEKTGAQLVVDAEKDLVETVLPYR-PLFIKPNKDELEVMFNTTVKSDEDVIKYGKE 211
                                                                                                                                 :: | :: : : | : : : | 212 ILKKGAQSVIISLGGDGAIYVDQ-----HQSIKAVNPQGHVVNTVGSGDSTVAGMVAGL 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 LTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLR------------VLSRN---QQL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 IR---LD-----FEEGFEGVDPQPLHERINQALSSIGALVLSDYAK--GALASVQQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 LRESELDVDLIKKATIFHYGSISLIDEPCRST-----HLAAMDIAKRSGSILSYDP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 MIQL-----ARKAGVPVLIDPKGTDFERYRGATLLTPNLSEFEAVVG-KCKTEEEIVE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 VMYVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGA-ANVAMNIASLGANARLVG 71
MIQLARKAGVPVLIDPKGTDFER---YRGATLLTPNLSEFEAVVG-KCKTEEEIVERGMK
                                                                                                      LIADYELSALLVTRSEQGMSLLQPGKAPLHMPTQA----QEVYDVTGAGDTVIGVLAATL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bennett, Alan B.
APPLICANT: Ranayama, Yoshinori
TITLE OF INVENTION: Fructokinase Genes and Their Use in
TITLE OF INVENTION: Metabolic Engineering of Fruit Sweetness
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RE-LEASE #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/826,611

FILING DATE: 05-APR-1997

CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 5.7%; Score 137.5; DB 3; Best Local Similarity 24.4%; Pred. No. 2.4e-05; Matches 85; Conservative 48; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 023070-077400US
                                                                                                                                                                                                                                          275 AAGNSLEEACFFANAAAGVVVGKLGTST 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFRENCE/DOCKET NUMBER: 02307
TELEPCOMMUNICATION INPORMATION:
TELEPHONE: (415) 576-0200
INPORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08826611
Patent No. 6031154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 347 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-826-611-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     US-08-826-611-2
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  163
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                                                                                              GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BPIDERAIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
FILE REFERENCE: GTC-007
CURRENT PILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-10-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: BY NOCETTE AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENCE: GTC-O07
CURRENT PILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
RIOR FILING DATE: 1997-10-08
RIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NOS: 5674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 KVVMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVL 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 GALEAVDWVVSFEEDTPQRL--IAGILPDLLVKGGDYKPEEIAGSKEVWANGGEVLVLNF 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GGAANVAMNIASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 SRNQQLIRLDFEEGFEGVDPQPLHERINQALSSI-----GALVLSDYAKGALAS--VQQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 GKGINVSRVLKTLDVDSTALGFSG-GFPGDFIAQTLEDSNIQSDFVQVDED---TRINVK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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21.6%; Pred. No. 2e-05;
Live 58; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 150; DB 4;
Pred. No. 2.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5583, Application US/09134001C Patent No. 6380370
                                                Sequence 5560, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Staphylococcus epidermidis US-09-134-001C-5583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.38;
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Best Local Similarity
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Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-134-001C-5583
                        US-09-134-001C-5560
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1439 ELTAQSGHKRHATLLRLVRAHAAAVLGQSSGDAVS-----SARAFRDLGFDSLTALELR 1492
                                                                                                                                                                                                                  1493 DRLSTSTGLK-----LPTSLVFD-----HSSPAALARHIGEELL----GRNDTADRAGPD 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1178 RGTVLIAGDL------TTVPGRLVRSLLE--DGADRVVLAGPDAPAQAAA 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1220 AGLTGVSLVPVRCDVTDRAALAALLDEHAPTVAVHAPPLVPLAPLRETAPGDIAAALAAK 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGFEG--VDPQPLHERINQALSSIGALVLSDYAKG-----ALASVQQMIQLAR 168
                                                                                                                                                                      -KLAVAAARKRGEKVVMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDS 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 VGLTGI------DDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 RAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARL 69
                                                                       271 AATLAAGNSLEEACF-FANAAAGVVVGKLGTSTVSPIELENAVRGRADTGFGVMTEEEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3724;
                                                                                                                                                                                                                                                                                                  RPVNPLEQEMIVLGALEAVDWVVSFEEDTPQRLIAGILPDLLVKGGD 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.6%; Score 134.5; DB 2, 24.0%; Pred. No. 0.0026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rao, Nagaraja R.
APPLICANT: Richardson, Mark A.
APPLICANT: Rosteck, Paul R., Jr.
TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: PAUL R. CANTRELL 1138
LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: Macintosh 7.0 SOFTWARE: Microsoft Word 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,198
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08804198 Patent No. 5945320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Burgett, Stanley G. APPLICANT: Kuhstoss, Stuart A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CANTRELL, PAUL R.
REGISTRATION NUMBER: 36,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3885
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3724 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 112; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-804-198-4
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                                                                                                                                                                                                                                                                      388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1280 TTAAGHLVDLAP------AAGLDALVLFSSVSGVWGGAAQGGYAAASAHLDALAERAR 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1178 RGTVLIAGDL------TTVPGRLVRSLLE--DGADRVVLAGPDAPAQAAA 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1332 AAGVPAFSVAWSPWAGGTPADGAEAEFLSRRGLAPLDPD----QAV----RTLRRMLERG 1383
                                                                                            --LKRLFHPNLKLLLVTEGSAGCRYYTKEFKGR----VNSIKVKAVDTTGAGDAFTGGVL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 VGLTGI-----DDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFE 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGFEG--VDPQPLHERINQALSSIGALVLSDYAKG------ALASVQQMIQLAR 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MK--LIADYELSALLVTRSEQGMSLLQPG----KAPLHMPTQAQEVYDVTGAGDTVIGVL 270
----MSVWNLADIIKISEDEISFLTGADDPNDDEVV- 238
                                              RGMKLIADYELSALLVTRSEQGMSLLQ---PGKAPLHMPTQAQEVYDVTGAGDTVIGVLA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAGVMVVGDVMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---IDPKGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERG
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                                                                                                                                             ATLAAGNS-----LEEACFFANAAAGVVVGKLGTSTVSPIELENAVR 313
                                                                                                                                                                    193 KCLASDASLYQDEKRLREAIFFANVCAALTV--TGRGGIPSLPTQDAVR 339
                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/08804227C
Patent No. 5876591
GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhaforss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INFUNION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 134.5; DB 2;
Pred. No. 0.0026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: FLOPPY disk
COMPUTER: ELOPPY disk
COMPUTER: IBM COMPALIDLE
COMPUTER: BW COMPALIDLE
COMPUTER: BW COMPALIDLE
COMPUTER: BW COMPALIDLE
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
FILING DATE: FEBTUARY 21, 1997
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REFERENCE/DOCKET NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: THOMAS G. PLANT 1501
LILLY CORPORATE CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.6%;
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Best Local Similarity 24.0%
Matches 112; Conservative
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NLRLPLWPSEDAARSGI-
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                                                                                                                                                                                                      1439 ELTAQSGHKRHATLLRLVRAHAAAVLGQSSGDAVS----SARAFRDLGFDSLTALELR 1492
                                    1332 AAGVPAFSVAWSPWAGGTPADGAEAEFLSRRGLAPLDPD----QAV----RTLRRMLERG 1383
                                                                                                                        1384 SACGAVADVEWS-----RFAASYTWVRPAVLFDDIPDVQRLRAAELAPSTGDSTTSELVR 1438
                                                                                                                                                               271 AATLAAGNSLEEACF-FANAAAGVVVGKLGTSTVSPIELENAVRGRADTGFGVMTEEEL- 328 '
                                                                                                                                                                                                                                                                         MK--LIADYELSALLVTRSEQGMSLLQPG----KAPLHMPTQAQEVYDVTGAGDTVIGVL 270
                                                                                                                                                                                                                                                 -KLAVAAARKRGEKVVMTNGVFDILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGDS 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 LSKS-----LADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFE-----EGFEGVD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 PQPLHERINQALSSIGALVLSDYAKGAL-----ASVQQMIQL--ARKAGVPVLIDPKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 ADYELSALLVTRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----LKAVL----EGAMDAGRNLFI-----DELHTMVGAGKA-----EGAMDAGNML 304
-----IDPKGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 PVHLLSALLEQQGGGSIKPLLMQVGFDIAALRSGLNKELDALPKİQSPTGDVNLSQDLAKL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVVKVNTIEERPGGA-----DDAARNIASL--GANARLVGLTGI------DDAARA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DPNVEESRQALDKYTVDMTKRAEEGKLDPVIGRDDEIRRTIQVLQRRTKNNPVLIGEPG
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REPERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
FRIOR APPLICATION NUMBER: US/09/199,637A
PRIOR APPLICATION NUMBER: US/09/199,637A
PRIOR PLIING DATE: 1998-11-25
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
                                                                                                                                                                                                                                                                                                                                 RPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRLIAGILPDLLVKGGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 281, Application US/09199637A
Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rahme, Laurence G.
Mahajan-Miklos, Shalina
Tan, Man-Wah
Cao, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ausubel, Frederick
Goodman, Howard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOFERYRGATLLTPNLS----
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169 KAGVPVL--
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SOFTWARE: FAST
SEQ ID NO 281
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT
                                                                               217
                                                                                                                                                                                                                                               329
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                                                                                                                                                                      388 RP--VNPLEQRMIVL----GALEAVDWVVSFEEDTPQRLIAGILPDLLVKGGDYKPEEIA 441
                                                                                                                                                                                               281 EEACFFANAAAGVVVGKL---GTSTVSP----IELENAVRGRADTGFGVMTEEELKLAVA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 NTIEERPGGAANVAMNIASLGAN-----ARLVGLTGIDDAARALSKSLADVNVKCDFVSV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKVTLPEFERAGVM-----VVGDVMLDRYWYGPTSRISPEAP----VPVVKV 43
                                                                                     34 AARKRGEK----VVMTNGVFDILHAGHVS--YLANARKLGDRLIVAVNSDASTKRLKGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cowart, Marlon Daniel, Halbert, Donald APPLICANT: Cowart, Jr., James F., McNally, Teresa TITLE OF INVENTION: Adenosine Kinase Polypeptides NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 117.5; DB 2;
Pred. No. 0.0026;
55; Mismatches 145;
                                                                                                                                                                                                                                                                                  442 GSKEVW-ANGGEVLVLNFEDGCSTINIIKKIQQDKK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: D-377 AP6D, 100 Abbott Park Road CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System 7.1
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 5749.US.DI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 937-4884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/479,614
FILING DATE: June 7, 1995
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MEDIUM TYPE: Diskette, 3.50 inch
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08479614 Patent No. 5861294 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.9%;
19.0%;
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Best Local Similarity 19.08
Matches 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tire.
TOPOLOGY: linea.
TROHLE TYPE: protein
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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ZIP: 60064-3500
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-----ARKAG 171
                                                                                                                                                                           172 VPVLIDPKGÜDFERYRGATLLTP--NLSEFEAVVGKCKTEEEIVERGMKLIADYELSALL 229
                                                                                                                                                                                                                                                                  252 F-----ETKDIKEIARKTQALPKVNSKRQRTVIFTQGRDDTIVATG-----NDVTAFP 299
                                                                                                                                                                                                                                                                                                        230 VTRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANA 289
                                                                                                                                                                                                                                                                                                                                  72 FKVEYHAGGSTQNSMKVAQWMIQEPHRAATFFGCIGIDKFGEILKSKAADAHVDAHYYEQ 131
                                                                                                               132 NEOPTGTCAACITGGNRSLVANLAAANCYKKEKHLDLENNWMLVEKARVYYIAGFFLTVS 191
44 NTIEERPGGAANVAMNIASLGAN----ARLVGLTGIDDAARALSKSLADVNVKCDFVSV 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08826611
Patent No. 6031154
GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Kanayama, Yoshinori
TITLE OF INVENTION: Fructokinase Genes and Their Use in
TITLE OF INVENTION: Metabolic Engineering of Fruit Sweetness
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 328;
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                                                                                                                                                     130 PQPLHERINQALS-----SIGALVLSDYAKGALASVQQMIQL---
                                                                         99 PTHPTIT-KLRVLSRNQQLI------RLDFEEG----
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; DB 3;
0.0031;
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Pred. No. 0
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APPLICATION NUMBER: US/08/826,611
FILING DATE: 05-APR-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.8%; Scc.
23.7%; Pred
51;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: PatentIn Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
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342 AASVIIRRTG 351
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Best Local Simmatches 80;
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 --FEGVD 129
                                                                                                 172 VPVLIDPKGTDFERYRGATLLTPNL-SEFEAVVGKCKTEEEIVERGMKLIADYELSALLV 230
                                                                                                                                                                           253 F-----ETKDIKEIAKKTQALPKMNSKRQRIVIFTQGRDDII-----MATESEVTAFAV 301
                                                                                                                                                                                                                            231 TRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAA 290
                                                                                                                                                                                                                                                  133 NEQPTGTCAACITGDNRSLIANLAAANCYKKEKHLDLEKNWMLVEKARVCYIAGFFLTVS 192
                                                                         130 PQPL-----HERINQAL--SSIGALVLSDYAKGALASVQQMIQL-----ARKAG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKVEAPEALSENVLFGMGNPLLDISAVVDKDFLDKYSLKPNDQILAEDKHKELFDELVKK 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKVTLPEFERAGVM-----VVGDVMLDRYWYGPTSRISPEAP----VPVVKV 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 361;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cowart, Marlon Daniel, Halbert, Donald N., APPLICANT: Kerwin, Jr., James F., McNally, Teresa TITLE OF INVENTION: Adenosine Kinase Polypeptides NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153;
99 PTHPTIT-KLRVLSRNQQLI------RLDFEEG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.9%; Score 116.5; DB 20.3%; Pred. No. 0.0032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: Abbott Laboratories
T: D-377 AP6D, 100 Abbott Park Road
Abbott Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPPERATING SYSTEM: Macintosh System 7.1 SOFTWARE: Microsoft Word 6.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/479,614 FILING DATE: June 7, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5749.US.DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 3.50 inch COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08479614 Patent No. 5861294 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
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REGIESTRATION NUMBER: 32,459
REFERENCE/DOCKET NUMBER: 57,
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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ADDRESSEE: Abbott La
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nes 75; Conserve
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Matches
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144 IGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPK-----GTDFER--YRGATLLTPN 195
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APPLICANT: Zalacain, Magdalena
APPLICANT: Zalacain, Magdalena
APPLICANT: Brown, James R.
TITLE OF INVENTION: No. 5861281el lacC
NUMBER OF SEQUENCES: 7
CORRESSEDDENCE ADDRESS:
ADDRESSE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 4.7%; Score 112.5; DB 2; Best Local Similarity 23.5%; Pred. No. 0.0061; Matches 76; Conservative 54; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              313 RGRADTGFGVMTEEELKLAVAAARKRGEKVVMT 345
                                                                                                                                                                                                                                                                                     302 GGSARHGEGRVRRGR----GGAARPRAGRPHMT 330
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Patent No. 5861281
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NAME: Dickinson, Q. Todd
REGISTRATION NUMBER: 28,354
REFRENCE/CDOCKET NUMBER: GMIC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215/994-2252
TELEFAX: 215/994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 303 amino acids
TYPE: amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                  126 ----EGVDPQPLHERINQALSSIGALVLSDYAKGAL-----ASVQQMIQLARKAGVPVL 175
                                                                                                                                         113 FYRNPSADMLLTPAELN--LDLIRSAKVFHYGSISLIVEPCRAAHMKAMEVAKEAGALLS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVSVPT-HPTITKLRVLSRNQQLIRLDFEEGFE------GVDPQPLHERINQALSS 143
                   67 ARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGF- 125
                                                                                                                                                                                                              171 YDPNLRLPLWPSAEEAKKQIKSIWDSADVIKVSDVELEFLTGSNKIDD----ESAMSLWHP 227
                                                                                                                                                                                                                                                                 223 YELSALLVTRSEQGMSL----LQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGN 278
                                                                                                                                                                                                                                                                                         71; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 VDGLEVRRGGVAVGIAFGLGRPGPTPLLVGAVGND-----FADYGTWPKEHGVDTG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 VNTIEERPGG-AANVAMNIASLGANARLVGLTGIDDAARALSKSLADV-----NVKCD 94
                                                                                                                                                                                  176 IDP------KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; DB 4; Length 366; 0.0042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.8%; Score 115.5; DB 4; Length 3 Best Local Similarity 25.5%; Pred. No. 0.0042; Matches 85; Conservative 31; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,957A
                                                                                                                                                                                                                                                                                                                                                   S-----LEEACFFANAAAGVVVGKLGTSTVSPIELE 309
                                                                                                                                                                                                                                                                                                                                                                                         282 TILEDEARLKEVLRFSCACGAITTTKKGAIPALPTASE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DeHOFF, Bradley S.
APPLICANT: ROSTECK Jr., Paul R.
TITLE OF INVENTION: SAM OPERON
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bil Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
COUNTRY: U.S.
ZID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INCORMATION:
TELEPHONE: 317-276-3334
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 46285
COMPUTER READABLE FORM:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-955-957A-3
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                                                                                       247 DVPVVDPTGIGAAFRAGFLAGAGRGLSIVSA----ARLGCVLAARALGTVGPADLPDRS 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 VMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGG-AANVA-----MNIASLGANARLVGL 72
144 ---LICPD---DPAAMVRHTAQ-CREPGLPFVADPSQQLARLETDEVRALVHGAHWVFTN
                                                    196 LSEFEAVVGKCKTEEEIVER-GMKLIADYE-LSALLVTRSEQGMSLLQPGKAPLHMPTQA
                                                                                                                                                                   254 Q-EVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSPIELENAV
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229 LVTRSEQGESLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFAN 288
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   131 QPLH-ERINQALSSIGA---LVLSDYAKGALASV--QQMIQLAKRAGVPVLIDPKG---- 180
                                                              109 EPVKLEELKAILSSLTAEDTVVFAGSSAKNLGNVIYKDLISLTRUTGAQVVCDFEGQTLI 168
                                                                                                                                                                --ARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTIT-KLRVLSRNQQLI----- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 KAATFFGCIGIDKFGEILKRKAAEAHVDAHYYEQNEQPTGTCAACITGDNRSLIANLAAA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 VVDKDFLDKYSLKPNDQILAEDKHKELFDELVKKFKVEYHAGGSTOKSIKVAQWMIQQPH 81
                                                                                                                               181 --TDFERYFGATLLTPNLSEFEAVVG-KCKTEEEIVERGMKLIADYELS-----AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 345;
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Patent No. 5861294

Sequence 1. Second No. 5861294

SEQUENCE CONTRIBERT CONTRIBERT OF THE CONTRIBERT OF THE CONTRIBERT OF THE CONTRIBERT OF THE CONTRIBER OF SEQUENCES: 34

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE
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4.7%; Score 111.5; DB 2;
Best Local Similarity 19.2%; Pred. No. 0.0096;
Matches 66; Conservative 51; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: Macintosh System 7.1
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,614
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CLASSIFICATION.
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MEDIUM TYPE: Diskette, 3.50 inch
COMPUTER: Macintosh
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NAME: Thomas D. Brainard
REGISTRATION NUMBER: 32,459
REFERENCE, DOCKET NUMBER: 5749
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708) 937-4884
TELEFAX: (708) 937-4884
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               AC-----GTATTFSDDLATA 288
                                                                                                                                                                                                                                                                                                                                                                                    289 AAAGVVVGKLGTSTVSPIELENA 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-08-479-614-5
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                                                                                                                                                                                                                                                 229 LVTRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFAN 288
                                                                                                                                                                                                                                                                                            131 QPLH-ERINQALSSIGA---LVLSDYAKGALASV--QQMIQLARKAGVPVLIDPKG---- 180
                                                          EPVKLEELKAILSSLTAEDTVVFAGSSAKNIGNVIYKDLISLTRQTGAQVVCDFEGQTLI 168
                                                                                                                                                         TGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFEGVDP-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 VMLDRYWYGPTSRISPEAPVPVVKVNTIEERPGG-AANVA-----MNIASLGANARLVGL 72
                                                                                                                        181 --TDFERYRGATLLTPNLSEFEAVVG-KCKTEEEIVERGMKLIADYELS-----AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09185826
Patent NO. 6171840
GENERAL INFORMATION:
APPLICANT: Zalacain, Magdalena
APPLICANT: Brown, James R.
TITLE OF INVENTION: NO. 6171840el lacC
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert, Price & Rhoads
STRRET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.7%; Score 112.5; DB 4;
23.5%; Pred. No. 0.0061;
ive 54; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/185,826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/961,539
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ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Q. Todd
REGISTRATION NUMBER: 28,354
REFERENCE/POCKET NUMBER: GM10.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 289 AAAGVVVGKLGTSTVSPIELENA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                               AC-----GTATTFSDDLATA 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 23.5
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 215/994-2222
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US-09-185-826-2
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ZIP: 19103-2793
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APPLICANT: Lynn Doucette-Stamm et al APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BPIDERANIDIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENCE: GTC-007

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-10-8

PRIOR FILING DATE: 1997-10-8

RIOR FILING DATE: 1997-10-8

RED ID NOS: 5674
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                                                                                           SEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEQGMSLLQPGKAPLHMPTQAQEV 256
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142 NCYKKEKHLDLEKNWMLVEKARVCYIAGFFLTVSPESVLKVAHHASENNRIFTLNLSAPF 201
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; Pred. No. 0.012;
53; Mismatches 109; Indels 166;
                                                                                                                                                                                                                                                                              257 YDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLG 299
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3900
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Best Local Similarity 17.6%;
Matches 70; Conservative 53
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

November 24, 2002, 23:15:54; Search time 31 Seconds (without alignments) 240.985 Million cell updates/sec Run on:

US-09-912-020-325 2393 1 MKVTLPEFERAGVMVVGDVM.......FEDGCSTTNIIKKIQQDKKG 477 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100480 seqs, 15661496 residues

Searched:

100480 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	App	App	. ₹	A.	A,	A,	A,	Α,	App	۲,	Α,	A,	A,	Ap	×	A,	V,	A .	Α,
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	599-	-020	-242	-242	-242	-242	-242	-242	599-	-242	-242	-242	-242	-245	-242	-242	-242	-242	-242
	-741	-912	-815	-815	-815	-815	-815	-815	-741	-815	-815	-815	-815	-815	-815	-815	-815	-815	-815
_	US-09-741-669-469	JS-09-912-020-325	JS-09-815-242-103	JS-09-815-242-13759	JS-09-815-242-1	JS-09-815-242-1	JS-09-815-242-10892	JS-09-815-242-1	JS-09-741-669-479	JS-09-815-242-10400	JS-09-815-242-1397	JS-09-815-242-13883	JS-09-815-242-10180	JS-09-815-242-5399	JS-09-815-242-12303	JS-09-815-242-1	JS-09-815-242-1	JS-09-815-242-1	JS-09-815-242-
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30 110 4.6 11877 10 US-09-861-289-6 Sequence 6, Appli 31 109:5 4.6 866 12 US-10-07-693-113 Sequence 113, App 32 109 4.6 866 12 US-10-07-693-113 Sequence 113, App 32 108 4.5 858 10 US-09-971-536-64 Sequence 11396, A 34 106 4.4 844 10 US-09-815-242-11497 Sequence 11396, A 36 106 4.4 164 10 US-09-815-242-11497 Sequence 11477, A 36 106 4.4 308 10 US-09-815-242-10775 Sequence 0, Appli 37 105.5 4.4 308 10 US-09-815-242-10775 Sequence 6, Appli 40 104.5 4.4 1165 9 US-10-075-460-6 Sequence 6, Appli 41 1165 10 US-09-887-052-4 Sequence 6, Appli 42 104.5 4.4 1165 10 US-09-887-052-4 Sequence 6, Appli 42 104.5 4.4 1165 10 US-09-887-052-4 Sequence 6, Appli 42 104.5 4.4 1165 10 US-09-887-052-4 Sequence 6, Appli 43 103 4.3 618 10 US-09-934-901-18 Sequence 18, Appli 44 103 4.3 618 10 US-09-934-901-18 Sequence 18, Appli 44 103 4.3 618 10 US-09-815-242-11133 Sequence 11133, A 4

Sequence 469, Application US/09741669 Sequence 469, Application US/09741669 Patent No. US20020022718A1 Patent No. US20020022718A1 Patent No. US20020022718A1 Patent No. US20020022718A1 APPLICANT: Forsyth, R. Allyn APPLICANT: Ohlsen, Kari L. APPLICANT: Ohlsen, Kari L. TITLE OF INVENTION: Genes identified as required for: TITLE OF INVENTION: Drolliferation of E. coli FILE REFERENCE: ELITAR 0.094 CURRENT FILING DATE: 2000-12-19 FRIOR APPLICATION NUMBER: US 60/173005 PRIOR PRICK APPLICATION NUMBER: US 60/173005 PRIOR FILING DATE: 1999-12-23 NUMBER OF SEQ ID NOS: 481 SEQ ID NO 469 LENGHH: 477 TYPE: PRT CORGANISM: Escherichia coli US-09-741-669-469	atch 100.0%; Score 2393; DB 10; Length 477; Cal Similarity 100.0%; Pred. No. 3.7e-191; 477; Conservative 0; Mismatches 0; Indels 0; Ga Mismatches 0; Indels 0; Ga Mismatches 0; Indels 0; Ga MKVTLPEFERACVWVGDVMLDRYWYGPTSRISPEAPVPVKVNTIEFERGGAANVAMNI AKVTLPEFERACKWVGDVMLDRYWYGPTSRISPEAPVPVKVNTIEFERGGAANVAMNI AKVTLPEFERACKWVGDVMLDRYWYGPTSRISPEAPVPVKVNTIEFERGGAANVAMNI ASLGANARLYGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQCIRLD ASLGANARLYGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQCIRLD FEEGFEGVDPQPLHERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDPKG	121 FEEGFEGVDPOPLHERINQALSSIGALVLSDYAKGALASVOOMIQLARKAGVPVLIDFKG 180 181 TDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSEGGMSLL 240 111111111111111111111111111111111111
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APPLICANT: Travick, John
APPLICANT: Frositi, Jamie M.
APPLICANT: Frositi, Jamie M.
APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Yamanoric, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA 001Dv1
CURRENT APPLICATION NUMBER: US/09/912,020
CURRENT APPLICATION NUMBER: 09/492,709
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SSOFTWARE: FastsEQ for Windows Version 3.0
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                                                                                                                                                  ANARKLGDRLIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
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                                                                                                                                                                                                                                                                                     Sequence 325, Application US/09912020 Patent No. US20020045592A1
                                                                                                                                                                                                                                                                                                                               APPLICANT: Zyskind, Judith
APPLICANT: Ohlsen, Kari L.
APPLICANT: Trawick, John
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Matches 477; Conservative
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US-09-912-020-325
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61 ASLGANARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD 120
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKARYOUSS

TITLE OF INVENTION: PROKARYOUSS

CURRENT FILING DATE: 2001-03-21

PRIOR PELING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,727

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/255,931

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16
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Pred. No. 3.7e-191;
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                                                                                                                                                                                                                                                                                                                                                              Sequence 10301, Application US/09815242 Patent No. US20020061569A1
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100.0%;
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Zyskind, Judith W.
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APPLICANT: Trawick, John D.
""". Carr, Grant J.
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Matches 477; Conservative
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ANARKLGDRIJIVAVNSDASTKRLKGDSRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL 420
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 STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-27
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SOFTWARE: FastSEQ for Windows Version 4.0
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Best Local Similarity
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                                                 STVSPIELENAVRGRADTGFGVMTEEELKLAVAAARKRGEKVVMTNGVFDILHAGHVSYL 360
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Tanamoto, Robert T.
APPLICANT: Xu. H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13759
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123 EGFEGVDPQPL--HERINQALSSIGALVLSDYAKGALASVQQMIQLARKAGVPVLIDP-- 178
                                                                                                            113 GGNGHLSPAVLARHEHLLEQ-----AQVVVCQLESPLETVGHVLRRAHALGKTVILNPAP 167
                                                                                                                                                                                                                                                                     EQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGV 293
                                                                                                                                                                                                                                                                                                    60 IGAVGNDGAGAMMTDLMSQDEINL-----TGVTTLEKTATGOAFIMVDNAGENSI 109
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                                                                                                                                                                        179 --KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVE---RGMKLIADYELSALLVTRS
                                                                                                                                                                                                  70 VGLTGIDDAARALSKSLA--DVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLD----
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APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: Tawick, John D.
APPLICANT: Tawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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22.8%; Pred. No. 1.3e-08;
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10892
LENGTH: 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10892, Application US/09815242 Patent No. US/200206051569Al GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                          294 VVGKLGTSTVSPI -- ELENAVRGRA 316
                                                                                                                                                                                                                                                                                                                                                                                                         284 SVTRLGAQTSIPSREEVERALVGEA 308
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CORGANISM: Enterococcus faecalis
US-09-815-242-10892
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Best Local Similarity 22.89
Matches 72; Conservative
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299
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                                                                                               OPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Haselber, KOUSTL
APPLICANT: ASSKING, Judith W.
APPLICANT: Syskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Tawaick, John D.
APPLICANT: Yamanoto, Robert T.
CURRENT PRILOR INVERS: US/09/815,242
CURRENT PILING DATE: 2000-05-23
PRIOR PRILOR FILING DATE: 2000-05-26
PRIOR PRILOR APPLICATION NUMBER: 60/250,57
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,635
PRIOR APPLICATION NUMBER: 60/253,635
PRIOR APPLICATION NUMBER: 60/253,938
PRIOR APPLICATION NUMBER: 60/253,938
PRIOR APPLICATION NUMBER: 60/250,338
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Pred. No. 4.7e-09;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11854, Application US/09815242 Patent No. US20020061569A1 PENERL INFORMATION: APPLICANT: Haselbeck, Robert
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US-09-815-242-11854
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Length 305; Indels

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EQ ID NOS: 481
FastSEQ for Windows Version 4.0
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Patent No. US20020061569Al
GENERAL INFORMATICN:
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Zyskind, Julith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
Xu, H. HOward
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Similarity 24.5%;
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Best Local Similarity 24...
Best Local Similarity 24...
77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Escherichia coli
US-09-741-669-479
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283 AIAVTRKGAÇPSVP 296
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SOFTWARE: FastSEQ for
SEQ ID NO 479
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APPLICANT:
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APPLICANT:
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QGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAG-NSLEEACFFANAAAGV 293
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                                                                                                ----KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVTRSE 234
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APPLICANT: Yangmoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PROKaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 05/191,078
PRIOR PELING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR PILING DATE: 2000-12-16
PRIOR PILING DATE: 2000-12-16
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11035
LENGTH: 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11035, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
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Zyskind, Judith W.
Wall, Daniel
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TVQRFGAQPSIPYQHE 301
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APPLICANT:
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Best Local S.
Matches 66
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67 ARLVGLTGIDDAARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFE 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 LIDP----KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 RSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANAAA 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 QNAGSLVVLGSINADHI ---- LNLQSFPTPGETVTGNHYQVAFGGKGANQAVAAGRSGAN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
259 VTGAGDTVIGVLAATLAAGNSLEEACFFANAAAGVVVGKLGTSTVSFIELE 309
                                 248 TTAAGDTFNGGFVTALLEEKSFDEAIRFGQAAAAISVTKKGAQSSIFTRQE 298
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                                                                                                                                                                                          Sequence 479, Application US/09741669
Patent No. US2002022718A1
GENERAL INFORMATION:
APPLICANT: FORSYLN R. Allyn
APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli
FILE REFERENCE: ELITRA.009Aranti APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 1090-12-19
PRIOR FILING DATE: 1999-12-23
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Pred. No. 1e-06;
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PRIOR APPLICATION NUMBER: 66/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PASSESQ FOR WINDOWS VERSION 4.0
SEQ ID NO 13376
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Salmonella typhi
US-09-815-242-13976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291 AGVVVGKLGTSTVS 304
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 IAFIACTGDDSIGESVRQQLATDNI------DITPVSVIKGESTGVALIFVNG-E 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 GVDPQPLHERINQALS-----SIGALVLSDYAKGALASVQQMIQLARKAGVPV 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 LIDP---KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVERGMKLIADYELSALLVT
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR APPLICATION NUMBER: 60/255,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PRIOR PRIOR DATE: 2001-02-16
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FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10406
LENGTH: 309
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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Yamamoto, Robert T.
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Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Escherichia coli
US-09-815-242-10406
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283 AIAVTRKGAQPSVP 296
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                                                                                    Gaps
                                                                                                                                                     28 PTSRISPEAPVPVVKVNTIEERPGGAANVAMNIASLGANARLV----GLTGIDDAARALS 83
                                                                                                                                                                                                                              24 PEGKLRCSAPV-----FEPGGGGINVARAIAHLGGTATAIFPAGGATG----EHLV 70
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        Length 310;
                                                                                Indels
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APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTON: Prokaryotes
FILE REFERENCE: ELITRA.011A
Ouery Match 7.0%; Score 167; DB 10; Best Local Similarity 27.1%; Pred. No. 1.5e-06; Matches 85; Conservative 36; Mismatches 115;
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16;

14;

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79 ARALSKSLADVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFE---EGFEGVDP----- 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 VTRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLAAGNSLEEACFFANA 289
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                                                                                                                                                                                                                                                                                                        Length 309;
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APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT PAPLICATION NUMBER: 05/09/815,242
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/205,848
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-22
PRIOR FILING DATE: 2001-22-26
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Best Local Similarity 25.4%; Pred. No. 8.2e-06;
Matches 80; Conservative 37; Mismatches 122;
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10180
LENGTH: 309
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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Zyskind, Judith W.
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Trawick, John D.
                                                                                                                                                                                                                            ; ORGANISM: Escherichia coli
US-09-815-242-10180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMKLIADYELSALLVTRSEQGMSLLQPGKAPLHMPTQAQEVYDVTGAGDTVIGVLAATLA 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVQQMIQLARKAGVPVLIDP --- KGTDFERYRGATLLTPNLSEFEAVVGKCKTEEEIVER 215
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APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Vanamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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Best Local Similarity 24.8%; Pred. No. 2.2e-06;
Matches 67; Conservative 39; Mismatches 134;
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13883
LENGTH: 309
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PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-13883
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US-09-815-242-10180
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                                                                                                                                                                                                                                                                                                                                                                                                                              60 ESIRYVDLVIPEKGWGQKEDDVEKFDV----DVFVMGHDWE-----GEFDFLKDKCEVIY 110
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: PROKARYOTES
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
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illarity 31.7%; Pred. No. 2.9e-05;
Conservative 29; Mismatches 48;
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5399
LENGTH: 132
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020061569A1
GENERAL INFORMATION:
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US-09-815-242-12303
                                                                                                    ; ORGANISM: Staphylococcus aureus US-09-815-242-5399
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Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: 2yskind, Judith W.
                                                                                                                                                                                                      Best Local Similarity
Matches 45; Conserva
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Salmonella typhi D
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Enterococcus faeca
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SUMMARIES
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AAT42063
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AAH81477
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ABQ21090
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-MODEL-franct-p2n.model -DEV-xlp
-MODEL-franct-p2n.model -DEV-xlp
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-MODEL-franct-0.1 -LGOPGL-0.
-LGOPGZI-J/USFTO_spool/VS09912020/runat_25112002_091428_24237/app_query.fasta_1.647
-UB-N_Geneseq_1011002 -QFMT-fastap -SUFFIX-p2n.rng -MINMATCH-0.1 -LGOPGL-0
-LGOPEXT-0 -UNITS-blts -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-USER-US0912020_CGGN_1_1 281_CRUNAX++ HEAPSTIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US0912020_CGGN_1_1 281_CRUNAX++ HEAPSTIZE-500 -MINLEN-0 -MINLEN-0 -LGPU-3
-NO_MANP - LARGEDGRRY -NGG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                               - nucleic search, using frame_plus_p2n model
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Database

Haemophilus influe

novel

03-AUG-2000

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AAA65809 to AAA65889 and AAA66058 to AAA66138 represent nucleotide sequences derived from Escherichia coli which inhibit E. coli proliferation. AAA65890 to AAA66055 and AAB15886 to AAB16040 represent nucleotide and protein sequences associated with E. coli proliferation. AAA66056 and AAA66057 represent primers used for sequencing E. coli proliferation inhibiting nucleotide inserts in an example from the present invention. Methods from the present invention. Methods from the present invention and be used to identify a proliferation-required gene in a microorganism, by contacting a microorganism with a proliferation-required gene activity inhibitory nucleic acid identified in another organism, and determining if inhibition occurs in the second microorganism. The nucleic acid sequences identified as being required for bacterial growth and proliferation, can
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                                                                                                                                                                 Novel polynucleotides and polypeptides associated with microorganism proliferation, used to identify inhibitors of bacterial growth and proliferation, for use in antisense therapy -
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                                                                                         Froelich
                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 328 A; 352 C; 447 G; 307 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                     used for antisense therapy for killing bacteria.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                  Claim 8; Page 146-147; 316pp; English.
                                                                                        Trawick J,
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                                                                (ELIT-) ELITRA PHARM INC
                                                                                        Ohlsen KL,
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                       161 GlnGlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGly
                             AlaValValGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle
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The present invention describes a purified or isolated nucleic acid
sequence (I) consisting essentially of one of the 93 nucleotide sequences
given in AAH81201 to AAH81204, where expression of the nucleic acid in a
microorganism is capable of inhibiting proliferation of a microorganism.

(I) have antibocterial and antibiotic activities, and can be used in
gene therapy. Expression of (I) in a microorganism inhibits proliferation
of the microorganism, and the manufactured antibiotic is useful for
cof the microorganism, and the manufactured antibiotic is useful for
cof the microorganism, and the manufactured antibiotic is useful for
cof the microorganism in a subject, specifically humans. The
nucleic acids that inhibit bacterial growth or proliferation can be used
as antisense therapeutics for killing bacteria. In addition to
therapeutic applications, the nucleic acid sequences complementary to
sequences required for proliferation can be used as diagnostic tools.

Croc example, nucleic acid probes complementary to proliferation required
sequences that are specific for particular species of microorganisms can
be used as probes to identify particular microorganism species in
clinical specimens. AAH81295 to AAH81488 to AAH81488 to AH881491

Crepresent oligonucleotides, which are used in the exemplification of the
                                                       ID NO:276
                                                                                 Escherichia coli; identification; proliferation; microorganism; antimicrobial; antibacterial; antibiotic; gene therapy; diagnosi bacterial growth inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                required for Escherichia or antimicrobial agents -
                                                       nucleotide sequence SEQ
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11 for screening for
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                                                       protein encoding
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proliferation, useful
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P-PSDB; AAG98421.
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                                                       Escherichia coli
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                 21-SEP-2001
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CTGGATCGTTACTGGTACGGCCCCACCAGTCGTATCTCGCCGGAAGCGCCGGTGCCCGTG 120 9 40 9 ValLysValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIle LeuàspàrgTyrTrpTyrGlyProThrSerArgilèSerProGluàlaProValProVal MetLysValThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMet Length: Matches: Conservative: Mismatches: Indels: US-09-912-020-325 (1-477) x AAH81477 (1-1434) 2.92e-211 2393.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match: Pred. No.: -Score: a

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GTTAAAGTGAATACCATCGAAGAAGTCCGGGCGGCGCGGCTAACGTGGCGATATC
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1201 GGGGCACTGGAAGCGGTCGACTGGGTAGTGTCGTTTGAAGAGGACACGCCGCAGCGCTTG 1260
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                                                                                                                                                                              Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; ds; prokaryotic cellular proliferation gene;
antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                  coli DNA for cellular proliferation protein #289.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind JW,
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26-MAY-2000; 2000US-207727P.
23-CCT-2000; 2000US-24278P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-25931P.
16-FEB-2001; 2001US-269308P.
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Xu HH;
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P-PSDB; AAU34708.
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Yamamoto RT,
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Mismatches:
Indels:
Sequence 1434 BP; 328 A; 352 C; 447 G; 307 T;
                                         Matches:
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                               2.92e-211
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Best Local Similarity:
Query Match:
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GlnGlnMetIleGlnLeuAlaArgLySAlaGlyValProValLeuIleAspProLysGly 180
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GAAGAAGCCTGCTTCTTTGCCAATGCGGCGGCTGGCTGGTGGTCGGCAACTGGGAACC 900
            IlealaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysProGluGluIle
                                                           LysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeu
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                                                                                                                                                                                                                                                                                  Salmonella typhi DNA for cellular proliferation protein #57
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
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2001US-269308P.
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16-FEB-2001;
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27-NOV-2000;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella neumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part
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                                                of.
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                                             New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                 Seq ID No 9661; 511pp; English.
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P-PSDB; AAU38165
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Genome; bacterium; Haemophilus influenzae; computer readable medium;

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Db 1596552 GAATTTAAGCAAGCAAAGTACTCGTATTAGGCGACGTGATGCTTGATCGTTATTGGTTC 1596493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the complete genome sequence of the bacterium Haemophilus influenzae strain Rd. The invention relates to a computer readable medium (CRM) having recorded upon it the complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence in a computer readable form, it is possible to identify genomic sequence in a computer readable form, it is possible to identify commercially important nucleic acid fragments and expression modulating fragments (EMFs) of the Haemophilus genome. The EMFs can be used to regulate the expression of a nucleic acid molecule. Vectors and altered organisms comprising the predicted ORFs can be used to produce any of the polypeptide fragments of the H. influenzae Rd genome.
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95US-0426787.
95US-0476102.
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Best Local Similarity:
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21-APR-1995;
07-JUN-1995;
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DD 1596252 TTACGTATTTTATCTCGTCATCAACAGCTGCGCCCTTGATTTTGAAGAAGATTTCAAT 1596193
                                                                 1596192 AATGTAGATTGCAAGGATTTATTAGCGAAGTTAGAAAGTGCGGTGAAAATTACGGTGCT 1596133
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                                        GlyvalAspProGlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIleGlyAla 146
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prokaryotic cellular proliferation, their use in identifying the genes; their use in the discovery of novel antibiotics, the essential consens their use in the discovery of novel antibiotics, the essential genes; their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella compendantae, Pseudomonas aeruginosa and Enterococcus facetalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery compounds nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence ancodes an essential prokaryotic cellular proliferation protein.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
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                                                                                                                                                          Pseudomonas aeruginosa DNA for cellular proliferation
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27-NOV-2000;
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26-MAY-2000;
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The invention relates to a genetically-engineered outer membrane vesicle (bleb) preparation from a Gram-negative bacterium for use as a vaccine. The blebs of the invention are improved with respect to their immunogenicity and toxicity by the introduction of one or more genetic changes to the chromosome of the bacterium from which the blebs are derived. The changes made include the upregulation of protective antigen expression, the downregulation of immunodominant non-protective antigen expression, and genetic changes which result in detoxification of the Lipid A moiety of lipopolysaccharide (LPS). The invention also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified Gram-negative bacterium; outer membrane vesicle; bleb; vaccine; genetically modified; protective antigen expression; LPS detoxification; LPS; lipid A; homologous recombination vector; immunisation; immunoprotective; non-toxic; paediatric; ds.
                                                                                                                                                                                               1138 ACTCGCCTGAAGGGCGTTGGCCGGCCGATCAACTCGGTGGACCGGCGCATGGCGGTACTC 1197
                                                                                                                                                                                                                                                                                                                                 1198 GCCGGGCTCGGCGCGGGGGCTGGGTGAGCTTCGCCGAAGACACTCCTGAGCGCCTG 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                Lobet Y;
                                                                                                                                                                                                                                                                                                                                                                                              440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae (HiRd) HtrB gene upstream sequence, SEQ ID:64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     оf
                                                                GAACAGGCGCGCCCCAGGGCGACCGCCTGATCGTCGGGGGTCAACGACGACGCCTCGGTC
AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr
                                                                                                                                                                                                                                                                   GlyAlaLeuGluAlaValAspTrpValValSerPheGluGluAspThrProGlnArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                 IlealaGlyIleLeuProAspLeuLeuValLysGlyAspTyrLysProGluGluIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441 AlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp
                                                                                                                                     LysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1378 AACAGCTCCACCACCGCCATCGTCGAGAAGATCCGCCAG 1416
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t P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyCysSerThrThrAsnIleIleLysLysIleGlnGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 46; Page 93-94; 128pp; English.
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Thonnard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF91438 standard; DNA; 1001 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JUL-2000; 2000WO-EP07424
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preparations are made, a vector suitable for performing recombination to preparations are made, a vector suitable for performing recombination cevents (for the generation of the modified bacterial strains).

Sacretarially-derived nucleic acid sequences used in such a vector, and an immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole cell vaccine suitable for paediatric use. The bleb preparation is useful in the manufacture of a medicament for immunishing a human host against a disease caused by infection of one or more of the following: Neisseria gnoorrhoeae, Haemophilus influenza, Moraxella catarrhalis, Pseudomonas aeruginosa, Chlamydia trachomatis, and Chlamydia pneumonia. The invention may also be used to provide immunisation against the influenza virus. Bacterially derived nucleotide sequences of the influenza virus used in the performance of homologous recombination events up to 1000 bp upstream of a bacterial chromosomal gene in order to either increase or decrease expression of that gene. Immunoprotective and non-toxic Gram-negative bleb, ghost, or killed whole cell vaccines are more immunogenic, less toxic and safer, and are particularly useful for paediatric use. The present sequence represents a specifically claimed Haemophilus influenzae nucleic acid sequence.
   strains from which the bleb
Gram-negative bacterial
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Sequence 1001 BP; 301 A; 225 C; 168 G; 307 T; 0 other;

3	מלחמ	; o Oction (1) of (2) of (2) of (3) o Oction (3) o		
Alignm Pred. Score:	Alignment Pred. No. Score:	: Scores: 2.86e-86 Length: 1036.00 Matches:		
Per(Best	cent S	Percent Similarity: 82.37% Conservative: 42 Best Local Similarity: 68.14% Mismatches: 52		
Oue: DB:	ry Mat	43.29% Indels:. 22 Gaps:		
0-SD	9-912	2-020-325 (1-477) x AAF91438 (1-1001)		
ò	7	7 GluPheGluArgAlaGlyValMetValValGlyAspValMetLeuAspArgTyrTrpTyr	ryr 26	
Q 0	886		82	7
ò	27	GlyProThrSerArglleSerProGluAlaProValProValValLysValAsnThrIle	Ile 46	
q	826		AAT 767	7
ò	47		Asn 66	
QQ	766	SAGAACGCGCGCGCGCGTGCTGCAAATGTGCCGATGAATATTGCTTCACTCAATGTACCC	ccc 707	7
Οy	67	7 AlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeu	ren 86	
đ	106		64	7
ογ	87	7 AlaAspValAsnValLysCysAspPheValSerValProThrHisProThrIleThrLys	Lys 106	9
q	646		58	7
ογ	107	/ LeuArgValLeuSerArgAsnGlnGlnCeuIleArgLeuAspPheGluGluGlyPheGlu	31u 126	9
q	586		AAT 527	7
ογ	127	7 GlyvalaspproGlnProLeuHisGluArglleAsnGlnAlaLeuSerSerIleGlyAla	14	9
Q	526		3CT 467	7
ογ	147	LeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIleGlnLeu	Leu 166	9
QQ	466		ATT 407	7
ογ	167	7 AlaArgLysAlaGlyValProValLeuIleAspProLysGlyThrAspPheGluArgTyr	ryr 186	9
QQ	406		34	7
οy	187	7 ArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPheGluAlaValValGlyLysCys	Cys 206	9
qq	346		rer 287	7
ογ	207	$^\prime$ LysThrGluGluGluIleValGluArgGlyMetLysLeuIleAlaAspTyrGluLeuSer	Ser 226	9

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The invention relates to an immunogenic composition comprising an antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived from a pathogen capable of protecting a bleb preparation derived from a pathogen capable of protecting a bleb preparation derived from a Gram-negative bacterial strain. The immunogenic composition consists of N. meningtidis B blebs or N. meningtidis C polysaccharide antigen. The blebs (derived from the outer membrane) may also have their toxic lipopolysaccharide (LPS) content reduced using heterologous down regulating sequences for LPS pathway genes or by up regulating genes involved in LPS synthesis suppression, by a promoter replacement technique. The immunogenic preparation is useful in the manufacture of a medicament for the treatment of a disease caused by the pathogen from which the antigen is derived (e.g. from Norsacia, meningtis and bacteraemia, from Morsacia, o.titis media and pneumonia, and from H. influenzae chronic bronchitis, sinustits, pneumonia, and otitis media). The bleb derived from M. catarrhalis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as.
                                                                                                                                     Upstream sequence; ds; Antibacterial; vaccine; bleb;
Gram-negative bacteria; outer membrane; LPS; lipopolysaccharide;
meningitis; bacteraemia; otitis media; pneumonia; chronic bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garcon N;
                                                                                                                                                                                                                         106 ATTAGTGTATTAGCAACCACATTAGCAGATGGACGTTCTTTCGAASAAFCTTGTTACCTA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New immunogenic composition comprising an antigen derived from a pathogen and a bleb preparation from Neisseria meningitidis, useful a vaccine for treating or preventing disease caused by the pathogen
227 AlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaPro
                                                                   267 IleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePhe
                                                                                                                   247 LeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGlyAlaGlyAspThrVal
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P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequence upstream of htrB #3 gene.
                                                                                                                                                                                                                                                                                                                                                  ABK37818/c
ID ABK37818 standard; DNA; 1001 BP.
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08-FEB-2001; 2001GB-0003170.
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106 ATTAGTGTATTAGCAACCACTTAGCAGATGGACGTTCTTTCGAAGAATCTTGTTACCTA 47

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from a non-typeable H. influenzae is useful as an adjuvant in an immunogenic composition comprising one or more pneumococcal capsular polysaccharides or protein antigens. The present sequence is an upstream sequence from an N. meningitidis, H.influenzae or M. catarrhalis gene involved in LPS biosynthesis, which either up regulates or down
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146
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                                                                                                                                                                                                                                       767
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                                                                                                                                                                                                                                                                                                                     GAAAAACAAAAGATTGATTGTAATTTTGTTGCATTAGAAACCCATCCAACCATTACTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 LysThrGluGluGluIleValGluArgGlyMetLysLeuIleAlaAspTyrGluLeuSer
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                                                                                                                                                                                                                                                                                                                                                                                                                  AlaAspValAsnValLysCysAspPheValSerValProThrHisProThrIleThrLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  526 AATGTAGATTGCAAGGATTTATTAGCGAAGTTAGAAAGTGCGGTGAAAATTACGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaArgLysAlaGlyValProValLeuIleAspProLysGlyThrAspPheGluArgTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 LeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGlyAlaGlyAspThrVal
                                                                                                                                                                                                                                                                                                                                                                     AlaArgieuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeu
                                                                                Sequence 1001 BP; 301 A; 225 C; 168 G; 307 T; 0 other;
                                                                                                                  1001
201
42
52
0
                                                                                                                                           Conservative:
Mismatches:
                                                           regulates sequences to which it is attached
                                                                                                                   Length:
Matches:
                                                                                                                                                                   Indels:
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1036.00
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method CC classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue cypes and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the the allows the invarience of cytosine methylation described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, cytosine methylation, 5'-CpG-3', uracil; cytosine, diagnosis, drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide for detecting cytosine methylation SEQ ID NO 7681.
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                AlaSerThrLysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMet 397
                                                                                                                                                                                                                                                                                                                         GlnArgLeuIleAlaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysPro 437
                                                                                                                                                                                                                                                               CGTGGTGAAAAAGTGGTGATGATTAACGGTGTTTTTGATATTTTGTACGTCGGGTACGTT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                         ArgGlyGluLysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisVal
                                                                          SerLeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyr
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert genomic cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the lasses of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (il) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

Mapplaton status of many C residues to be determined simultaneously.

Mapplaton status of many C residues to be determined simultaneously.

Mapplaton status of the invention.
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                                                                                                                                                                                    Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA.
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Matches:
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ArgGlyGluLysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisVal

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WO200218632-A2

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Scarlato V;
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                  TTTTATTTGGTAAATGTTCGTAAGTTGGGTGATCGTTTGATTGTTGTTGTTATTATAGCGAT
SerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAsp
                                                                     418 GlnArgLeuIleAlaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleotide sequences of Neisseria meningitidis which can used in the diagnosis and treatment of N. meningitidis infection other Neisserial infections, for example, N.gonorrhoea -
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Scarselli
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Ratti G, Sc
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and antibodies
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                                                                                                                                                                                                                                                                                                  Sequence 78845 BP; 19372 A; 21111 C; 19042 G; 19318 T; 2 other;
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49
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Conservative:
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Indels:
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753.50
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                                                                                                                                                                                                                         45969
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Rappuoli R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine; diagnosis; antigen; detection; infection; gene therapy; antibacterial;
 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections - \,
                                                                                    GCCGGAATGGGTTGGGGTTTGGCGGCAGGCTGCATGCCCGAAGCCATGTACCTTGCC
LeuLeuValThrArgSerGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeu
                                 GTTTTACTGACCCGAAGCGAAGAAGCCATGACCTTGTTCAGCGAAGGCGAA---CCGATT
                                                                   HisMetProThrGlnAlaGlnGluValTyrAspValThrGlyAlaGlyAspThrValIle
                                                                                                                                    GlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAla
                                                                                                                                                                                                     AsnAlaAlaAlaGlyValValValGlyLysLeuGlyThrSerThrValSerProIleGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis B nucleotide sequence SEQ ID NO:109
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Scarlato V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peterson J, Tettelin H,
Ratti G, Scarselli M,
                                                                                                                                                                                                                                                                                                        TTGATCAAGGCATTGTCAGGGCAATCA 45762
                                                                                                                                                                                                                                                                        LeuGluAsnAlaValArgGlyArgAla 316
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                                                                                                                                                                                                                                                                                                                                                                          AAF21608 standard; DNA; 349980 BP.
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08-OCT-1999; 99WO-US23573.
28-FEB-2000; 2000GB-0004695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-2000; 2000WO-US05928
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Galeotti C, Mora M,
Frazer CM, Grandi G;
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due to Neisserial bacteria or as a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria. Computers, computer memory, computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently
preventing infection
                                                                                                                                                                                                                                                                                                                                                                                                                           247944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247945 GATGTGTCCCGTATTTCGCCCGAAGCCCCGTGCCGTGGCGAAAATCGGACGAATGGAC 248004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248185 CGCGTCGTCGCCCGCAACCAGCGTCTTATCCGTCTTGATTTTGAAGAACATCCCAACTGC 248244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248365 AAACACGCCGGCAAAACCGTCTTAATCGACCCCAAAGGCGACGATIACGAAAAAATATGTC 248424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248245 GAAGTGTTGGAACAAATCAAGCAGAAATACCGCGAAATTGCCCGAATACGACGCAATTC 248304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 ThrGluGluGluIleValGluArgGlyMetLysLeuIleAlaAspTyrGluLeuSerAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 ValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIleGlnLeuAla
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                                                                                                                                                                        G; 87805 T; 0 other;
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49
100
used in compositions for treating
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Mismatches:
Indels:
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Matches:
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753.50
67.31%
51.46%
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                       248721
                                                                        248781
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                                               307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptide encoded by operon including virulence genes of Neisseria meningitidis, useful as vaccine component for treating or preventing meningitis and for identifying antimicrobial drug
                                                            248722 AATACTGCGGCGCGGGGTTGTCGTGGCGAAACTCGGTACGCCGGTTTGCTCGTTTGCCCGAA
268 GlyvalLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAla
                GCCGGAATGGGCTTGGGTTTGGCGGCAGGCTGCCACCATGTACCTTGCC
                                                 AsnAlaAlaAlaGlyValValValGlyLysLeuGlyThrSerThrValSerProIleGlu
                                                                                                                                                                                                                                                                     Meningitis; virulence; gene; antibacterial; vaccine; veterinary; infection; Gram-negative bacteria; antimicrobial; ds.
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156
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103
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                               Neisseria meningitidis virulence gene #26
                                                                                                              Db 248782 TIGATCAAGGCAITGTCAGGGCAATCA 248808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 110-112; 423pp; English
                                                                                              LeuGluAsnAlaValArgGlyArgAla 316
                                                                                                                                                                        BP.
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745.50
66.34%
50.49%
31.15%
                                                                                                                                                                       AAS97221 standard; DNA; 969
                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-2001; 2001WO-GB02003
                                                                                                                                                                                                                                                                                                                                                                                                            38-MAY-2000; 2000GB-0011108
                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   (MICR-) MICROSCIENCE LTD
                                                                                                                                                                                                                                                                                                           Neisseria meningitidis
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P-PSDB; AAU72936.
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Indels:

Best Local Similarity:

Query Match:

Percent Similarity:

US-09-912-020-325 (1-477) x AAS97221 (1-969)

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PheGluArgAlaGlyValMetValValGlyAspValMetLeuAspArgTyrTrpTyrGly
                                                                                                                                                                                                                                                                                                                                                                                                                           48 GluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAla
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Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope; ds.
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Helicobacter pylori.

1.1272 /*tag= a /note= "no stop codon given in sequence" Location/Qualifiers : Key

WO9640893-A1

19-DEC-1996

96WO-US09122. 06-JUN-1996; 96US-0630405. 95US-0487032. 01-APR-1996; 07-JUN-1995;

(ASTR) ASTRA AB

, Mellgaerd BL; Berglindh OT, Smith D,

WPI; 1997-052306/05.

P-PSDB; AAW20763

Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter

Claim 9; Pages 847; 1481pp; English.

The present sequence encodes a Helicobacter pylori cytoplasmic protein. The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypetide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (APCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.

Sequence 1272 BP; 412 A; 232 C; 284 G; 344 T; 0 other;

Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 2.56e-58 734.50 58.66% 40.88% 30.69% Percent Similarity: Best Local Similarity: Query Match: DB: Alignment Scores: Pred. No.: Score:

US-09-912-020-325 (1-477) x AAT68016 (1-1272)

51 GlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLeuVal 70 ò q

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- GGGGTAGTGGGAGATGATTTAAAAGGCAAGCATTTCATTAGCACTTTAAATTCTATAAGG 126 71 GlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeuAlaAspValAsn 90 29

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- g
- 91 ValLysCysAspPheValSerVal---ProThrHisProThrIleThrLysLeuArgVal 109

Oy Dp	110 Leus	SerargAsnGlnGlnLeuIleArgLeuAspPheGluGluGlyPheGluGly ::::: ::::: 3CGCAAAACCAGCAAATCGTGCGCTGGATAAGGAAATC	
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QQ	235 CCC	TAAAACGCTGATTTAAGAAGAATCTTTAGATTTTATCGCAGAAAAATTCAAGAA 294	4
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Oy Op	355 ACC	WeTILeGInLeuklaArgLysAlaGIyValProValLeuILeAspProLysGLyThr 181 :::	7 2
Qy	182 Aspl	ابر PheGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPheGluAla 201	1
qq	111 415 GAT	::: ::: ::: ;::	4
Qy	202 Val	valGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIleAla 221	21
qq	475 GCG	TTCCATTTGAAATTAGACAGCCATGCGAATTTATCAAAAGCGCTCCAAATTTTACAA 534	4
δλ	222 Asp	TyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeu 240	0
οqα	535 GAA	ACTIAICATATCGCTATGCCTTTAGTAACCTTGAGCGAACAACGCATCGCTTTTTTA 594	34
Qy	241 Glni	ProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr 260	00
qα	595 GAA	AAAGGGGAGTTAGTCAATTGCCCCACTATGGCTAAGAAGTTTATGATGTAACG 651	13
Qy	261 Gly	*AlaGlyAspThrVallleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu 280	000
qq	652 GGG	SCAGGCGATACGGTGATAGCGTCTTTAACGCTCTCTTTATTGGAATCAAAAAGCTTG 711	=
Qy	281 Glu(00
qq	712 AAA(SAAGCTTGCGAGTTTGCTAATGCGGCTGCGGGGGGGGGGG	7.
δλ	301 Ser	ThrValSerProIleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPhe 320	02
qq	772 GCG	TTAGCGAGTTTAGAAGAAATCGCTTTGATTTTGAACCAAACGCACCCT 822	22
٥y	321 Gly	ValMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaAkgLysArgGlyGlu 340	9
QQ	823 AAA	ATCCTCCCTTTAGAAAAGCTGTTAGAAACTTTAGAACGCAACCAGCAA 873	73
Οy	341 Lys	ValValNetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSetTyrLeu 360	00
g	874 AAA	ATCGTTTTCACCAATGGCTGTTTTGATATTCTCCATAAAGGGCATGCGAGCTATTTG 933	33
Qy	361 Ala	AsnalaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr 380	00
qq	934 CAA	AAGGCTAAAGCTTTAGGGGATATTCTTGTTGTGGGGGTTAAATAGCGATAATTCCATT 993	33
ΟŊ	381 Lys	ArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeu 400	8
qq	994 AAA		53
Οy	401 Gly	AlaLeuGluAlaValAspTrpValValSerPheGluGluAspThrProGlnArgLeu 420	20
QQ	1054 GCG	AGCTTGTCTTGCGTGGTTTTGTGGTGTTTTGGAGAAGACACGCCCATAAAATTG 111	113
ΟŊ	421 Ile		
Q	1114 ATT		173
οy	441 Ala	3]ySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPheGluAsp 460	00
QQ	1174 ATA	GGGAGCGAGTTGGCTAAAGAACCCGTTTGATAGAATTTGAGAA 122	221
οy	461 Gly	yCysSerThrThrAsnIleIleLysLysIleGlnGln 473	

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Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
                                                                                                                 Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                   Oligonucleotide for detecting cytosine methylation SEQ ID NO 7683.
Claim 12; 56pp + Sequence Listing; 56pp; German.
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                                                                                                                                                                                                                                                                                       Berlin
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                                             ABQ21092 standard; DNA; 707
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05-SEP-2000; 2000DE-1044543.
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                                                                                  (first entry)
                                                                                                                                                                                                                                                                                      Piepenbrock C,
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                                     4BQ21092,
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-cpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic C Cytosine (C) but not methylated to two classes, each with at least one member, of oligonaleotides and/or peptide nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the member, of oligonaleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide colymorphisms (SNP's); and (ii) for differentiation of cell or tissue cypes and for investigating cell differentiation. The method allows the methylation status of many c residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method allows the contral column of the degree of cytosine methylation described in the chance of the contral column of the degree of cytosine methylation described in the column of the column

Sequence 707 BP; 137 A; 62 C; 178 G; 329 T; 1 other;

the invention

the disclosure of

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707
133
47
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       Length:
Matches:
Conservative:
Mismatches:
                                       Indels:
      4.25e-55
696.00
76.60%
56.60%
29.08%
                              Similarity:
                      Percent Similarity:
Alignment Scores:
                                      Query Match:
                              Best Local
        Pred.
                Score:
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US-09-912-020-325 (1-477) x ABQ21092 (1-707)

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257
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            AsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLys
                                                                                                                                  LeuGlyThrSerThrValSerProIleGluLeuGluAsnAlaValArgGlyArgAlaAsp
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                                                                                                            AATTCGCTAAAAAAACCTACTTCTTTACCAATACGACGACTAACGTAATAATCGACAAA
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Search completed: November 26, 2002, 21:16:52 Job time : 1025 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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November 26, 2002, 10:25:42; Search time 2404 Seconds (without alignments) 3213.497 Million cell updates/sec
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OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                        16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                 Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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2393
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Perfect score:
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Command line parameters:
-MODEL-frame+plan.model -DEV-Xlp
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-MODEL-frame+plan.model -DEV-Xlp
-OB-Cgn2_1/USPTO_spool/US09912020/runat_25112002_091428_24259/app_query.fasta_1.647
-OB-Cgn2_1/USPTO_spool/US09912020/runat_25112002_091428_24259/app_query.fasta_1.647
-OB-CGN2_1/USPTO_SPOOL/US08_DEV_NOTERNATA_00
-UNINS-blie -START=1 -END--1 -MATRIX-blosum62 -TRANS-human40 cd1 -LIST-45
-DOCALIGN-200 -THR.SCORE-PLANX-100 -THR_MIN-0 -ALKEN-15 -MODE-LOCAL
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-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT=0.5 -FGAPOP-6 -FGAPEXT=7 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

em_gss_mus:*
em_gss_other:*
em_gss_pro:*
em_gss_rod:* gb_gss:* em_gss_hum:* em_gss_inv:* em_gss_vrt:* em_gss_fun:* em_gss_mam:* em_estfun:* em_esthum:* em_estin:* em_estmu:* em_estpl:*
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gb_estl:*
gb_est2:*
gb_htc:* em_estom:* gb_est3:*
gb_est4:*
gb_est5:* em_estba:* em_estov:* EST: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	33	BH390803 AG-ND-140 BM167110 EST569633	BI786239 sai34e10.	Mus mus	BQ850159 QGB11007.	BM169900 EST572423 BJ165221 BJ165221	BI944705 sad41d05. BO995975 OGG11110.	BI308004 EST529414	BF642033 NF014A09I BG140383 EST480825	BJ435742 BJ435742	BJ428649 BJ432922 BJ432922	BJ432289 BJ432289	BF154250 057F11 Ma	BJ432465 BJ432465 BJ377283 BJ377283	BJ431261 BJ431261	BJ3/233/ BJ428867 BJ428867	AI995602 701675044	BU455210 BU45518 AV828468 AV828468	BG88833 EST514684	BG131085 EST463977	BM093385 saj08d02. BE920533 EST424303	BG145720 uu90b08.x	BG440694 GAEa000 BM358455 GAEa000	BQ198857 UI-R-EBO-	B142/212 sah/7106. A1326806 mj16e06.x	maa60g10	AWZ1904Z EST3015Z4 BI639334 SD21893.5	UI-R-BJ1	S	mRNA linear EST 14-JUL-2000 lus cDNA clone IMAGE:3216101 3' ADP-HEPTOSE SYNTHASE ;, mRNA		Vertebrata, Euteleostomi	ai :
SOU	BE332786 BH404405	вн390803 ВМ167110	BI786239	AK017229	BQ850159	BM169900 BJ165221	BI944705 BO995975	BI308004	BF642033 BG140383	BJ435742	BJ428649 BJ432922	BJ432289	BF154250	BJ432465 BJ377283	BJ431261	BJ428867	AI995602	AV828468	BG88833	BG131085	BM093385 BE920533	BG145720	BG440694 BM358455	BQ198857	BI427212 AI326806	BF453934	AWZ19042 BI639334	BE100952	ALIGNMENT	505 bp Mus muscu LI P76658	23	hordata;	odentia; S Kucaba,T.
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                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="primary sorted bone marrow cells"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/note="vector: pZL1; Site_1: Sal1; Site_2: Eag1; CDNA made
Sy oligo-dT priming Library amplified by stretch PCR.
Subtraction method: Bonaldo, et al., Genome Research
6:791. Library constructed by Dr. Archibald Perkins (Yale
University)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AG-ND-140M3.TR.1 ND-TAM Anopheles gambiae genomic clone AG-ND-140M3 bH404405
 Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person F., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1066249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 CTCGACCGTTACTGGCATGGTGGTACCTCACGGATTTCTTCTGAGGCGCCGGTGCCTGTG 367
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                                                                                    Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Feb: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetLysValThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMet
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Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                   Possible reversed clone: similarity on wrong strand
Seg primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                         /db_xref-"taxon:10090"
/clone="IMAGE:3216101"
/clone_lib="Perkins LRH"

    .505
    /organism="Mus musculus"

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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                            /strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                      /sex="female"
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82.56%
67.44%
12.12%
                                                                            Unpublished (1999
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Best Local Similarity:
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Shetty, J., Malek, J., Koo, H., Collins, F., Gardner, M. and Loftus, B.J. Direct Submission of BAC-end sequences from Anopheles gambiae (Unpublished (2001)) Other_GSSs: AG-ND-140M3.TF.1
                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extraced from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII Seq primer: M13 Rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThrHisPro 102
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                    Anopheles gambiae
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 LeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeu
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                                                                                                                                                                                                                                                                                                                             USA
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131 t
                                                                                                                                                                                                                                                                       Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
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/clone="AG-ND-140M3"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                     Contact: Brendan J Loftus
African malaría mosquito.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.11e-16
233.00
62.75%
47.06%
9.74%
                                                                                                                        (bases 1 to 483)
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LOCUS

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mena isolated using oligo(dT)-cellulose chromatography. First strand cDAA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to After packaging, the phagemid vector (pAD-GAL4) was excised from the HybrilaAP vector and plasmid DNA.
                                                                                                                                                                                                                              BM167110 502 bp mRNA Linear EST 04-DEC-2001
EST569633 PyBS Plasmodium yoelii yoelii cDNA clone PYCOC88 5' end,
mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_Stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
//note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByd mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the quantidinium isochiocymantematoria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: carlton@tigr.org
Sor clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
                                                                                                                                                                                                                                                                                                                                                                      Plasmodium yoelii yoelii
Bukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (Dases 1 to 502)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
Fraser, C.W. and Carucci, D.J.
Plasmodium yoelii EST project at TIGR
                                     82 uSerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThrHisPr 102
130 ACTTGGTGTAAAGGTTGGTCTTATTGGTGTTGGTGATGACGAAGCTGCCAGTACGAT 71
                                                                        70 TGAGGAATTGCTGACAAAAACAAATTGATGCGAAGCTAAGGCA FGATCCGTCGATATC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      502
36
36
36
36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Jane Cariton
Parasite Genomics Group
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:73239"
/clone="PYCOC88"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="PyBS"
                                                                                                                                                                                                                                                                                                                                                      Plasmodium yoelii yoelii.
                                                                                                                                                                                                                                                                                                               BM167110.1 GI:17300342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="17XL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.33e-10
179.00
50.31%
27.95%
7.48%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: ADF
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Best Local Similarity:
                                                                                                               102 oThrile 104
                                                                                                                                                                                                                                                                                            BM167110
                                                                                                                                                    10 GACAATT 4
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                BM167110
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                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                      BH390803 11-DEC-2001 SAG bp DNA linear GSS 11-DEC-2001 AG-ND-140M3.TR ND-TAM Anopheles gambiae genomic clone AG-ND-140M3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bloftusetigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas ABM Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 GTGACGACCATGGAAGTAACTGAAAAGCGCTTGCTGGTTGCAGGGGATATTATGGCTGGA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMet-LeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
| 150 c 105 g 147 t
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Matches:
Conservative:
Mismatches:
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/strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:7165".
/clone="AG-ND-140M3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                         African malaria mosquito.
                                                                                                                                                  внз90803.1 GI:17336944
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220.00
62.14%
46.60%
9.19%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: M13 Rev
Class: BAC ends.
                                                                                                                                                                                                                                                                                          bases 1 to 550)
                                                                                                                                                                                                                Anopheles gambiae
                                                                                                                 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                       Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                                                                                                         GSS.
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KEYWORDS
SOURCE
ORGANISM
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                                   RESULT 3
BH390803/c
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                                                                                          DEFINITION
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AUTHORS
TITLE
JOURNAL
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FEATURES

DRIGIN

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COMMENT

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/ndc="Vector: pBluescript II SK+; Site_I: ECORI; Site_2:
XhoI; The CDNA library was constructed from mRNA isolated
germinating shoots of the cultivar Killiams. The seeds
were allowed to germinate for 24 hours prior to being
cold stressed for 2 days at 4C. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. ECORI
adapters were ligated to the blunt-ended CDNA fragments
followed by XhoI digestion. The CDNA fragments were
directionally cloned into the ECORI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This library
was constructed in the laboratory cf Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ996249 652 bp mRNA linear EST 22-AUG-2002 QGG12F01.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGlyThr 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MetLysLeulleAlaAspTyrGluLeuSerAla-----LeuLeuValThrArgSerGlu 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 CAAGICGCACAGGCIGCAAGGAAIGCIGGCGIGCCAGIAGIGITIGAIGCGGGGGGGCAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluPheGluAlaValValGly---LysCysLysThrGluGluGlufleValGluArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :::||||
259 TTGAAATGC-----CATGAATTGGGAGTTAAGCAAGTTCTTGTGAAACTTGGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThr -- GlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 GlnGluValTyrAspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyVal
                                                                                                                         /clone_"GENOME SYSTEMS CLONE ID: Gnt-c1065-5204"
/clone_lib="Gn-c1065"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  555
54
20
67
11
5
                                                                                                                                                                        /tissue_type="germinating shoots"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGTTCAAGTGAAGGGAGCCTCTCCTAGCATGCCT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
                                                                                    /organism="Glycine max"/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-912-020-325 (1-477) x BI786239 (1-555)
Seq primer: -40RP from Gibco
High quality sequence stop: 421.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178.50
48.68%
35.53%
7.46%
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Pred. No.:
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ORIGIN
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BQ996249
                                              FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI786239 555 bp mRNA linear EST 30-NOV-2001 sai34e10.yl Gm-c1065 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1065-5204 5' similar to TR:Q9SHH5 Q9SHH5 F20D23.14 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                355
                                                                                                                                                                                                                                      395
                                                                                                                                                                                                                                                                                                                      408
                                                                                                                                                                                                                                                                                                                                              436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---ProGluGluIleAlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuVal 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      422
                                                                                                        AAAAAAAAGCATCATAAAGTTGTATATGTAGATGGATCATTTGATATGTTCCATTTAGGA 101
                                                                                                                                                HisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsn 375
                                                                                                                                                                          ValValSerPheGluGluAspThrProGlnArgLeuIleAlaGlyIleLeuProAspLeu 428
                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCATAACA-------GAAAGTTTTATTAAACGCTTTCAAATTGACACA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                ArgLysArgGlyGluLysValValMetThrAsnGlyValPheAspIleLeuHisAlaGly
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Public Soybean EST Project
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Qy 345 ThrasnGlyValPheaspile		381	Oy 412PheGLuGLuAspInrProc 	Db 501 GATGGAACTGACGCATATGCCC Qy 441 AlaGlySerLysGluValTrpA Db 552	Qy 461 GlyCysSerThrThrAsnIle1	RESULT 7 AK01729 LOCUS DEFINITION MUS MUSCULUS AGULT IN ENTIRCHED LIBRARY, CI INSERT SEQUENCE. ACCESSION AK01729.1 GI:12856 KEYWORDS HTC; CAP, Trapper. SOURCE MUS MUSCULUS (STRAIT MRA, Clone_LID:RIKE CLONE_LID:RIKE CLONE:STATE CLONE:S	•	JOURNAL Genome Kes. 10 (10), MEDLINE 2049974 PUBMED 11042155 REFERENCE 3 AUTHORS Shibata,K., Itoh,M., Konno,H., Akiyama,J. Sumi,N., Ishii,Y., N	Fujiwake,S., Inoue,P Yoneda,Y., Ishikawa, Okazaki,Y., Muramatte TITLE RIKEN integrated sec sequencing pipeline JOURNAL Genome Res. 10 (11), MEDLINE 20530913
QGG12F01, mRNA sequence. ACCESSION BQ996249.1 GI:22430645 KEYWORDS EST. SOURCE Lactuca sativa. ORGANISM Lactuca sativa. Eukarvota: Viridiplantae: Streptophy#a: Embryophyta: Tracheophyta:	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae; Lactuca. REFERENCE 1 (bases 1 to 652) AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison	,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K. TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project	Intep://compgenomics.ucdavis.edu/ JOURNAL Unpublished (2002) COMMENT Contact: Alexander Kozik [R.W.Michelmore] Department of Vegetable Crops, R.W.Michelmore Lab University of California at Davis (UCD) Asmindson Hall, HCD, Davis, CA 95516, HCA	Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659 Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QG_CA_Contig5995, see http://cgpdb.ucdavis.edu/ for details. Plate: OGG12 row: F column: 01.	FEATURES Location/Qualifiers source 1652 /organism="Lactuca sativa"	OUNT 182 a	Alignment Scores: 4.67e-10 Length: 652 Pred. No.: 178.00 Matches: 64 Score: 178.00 Conservative: 27 Best Local Similarity: 30.33% Mismatches: 60 Query Match: 7.44% Indels: 60 DB: 14 Gaps: 8	US-09-912-020-325 (1-477) x BQ996249 (1-652) Qy 297 LysLeuGlyThrSerThrValSerProIleGluLeuGluAsnAlaValArg 313 :: :: :: Db 39 AAGATGGGTTCGGATACAGGTCTAGAGAACTCGAAGCGGTTTCTAGCG 86 Qy 314GlyArgAlaAspThrGlyPheGlyValMetThr 324	87 ACATGGTTG 325 GluGluGlu 111 147 CCGGAGCTC

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h.M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., ma,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Ktsumoco,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., ioue, K., Togawa,Y., Izawa,M., Chara,E., Watahiki,M., Rawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Ramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. d sequence analysis (RISA) system--384-format line with 384 multicapillary sequencer
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Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
subtraction of cap-trapper-selected cDNAs to
h cDNA libraries for rapid discovery of new genes
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1. .1031
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                                    Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Alzawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Gazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischman, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Marchlonni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Toyo-oka, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RTKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Center (SCC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Stangawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL.http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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    .1031
    /organism="Mus musculus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: Mobile Clark NIL was constructed and seed was provided by Dt. J. Specht, University of Nebraska (Shoemaker and Specht, University of Nebraska (Shoemaker and Specht, University of Nebraska (Formand Trom Whole Seedlings of I week old greenhouse Isolated from whole Seedlings of I week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended CDNA fragments followed by XhoI digestion. The CDNA fragments were directionally cloned into the EcoRI xhoI restriction site of the pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-433 or contact via email: ccu@resgen.com
seq primer: -40RP from Gibco
High quality sequence stop: 409.
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                                                                                                                                                                                                                                                                                                                                         B1943547 572 bp mRNA linear EST 06-DEC-2001 sq63e05.yl Gm-c1048 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1048-153 5' similar to TR:Q9SHH5 Q9SHH5 F20D23.14 PROTEIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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/dev_stage="1 week old"
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yValLeuAlaAlaThrLeuAla-----AlaGlyAsnSerLeuGluGluAlaCysPhePh 286
                                                                                                                                               850 AGCGCTGGCCTTCTACCTGGCTTACTACCCAAATCTGTCCTTGGAAGAAATGCTCAAGAG 909
                                                                                                                                                                                               eAlaAsnAlaAlaGlyValValValValGlyLysLeuGlyThrSerThrValSerPro 305
                                                                                                                                                                                                                                         910 ATCCAATITICATCGCIGCAGICAGTGTACAGGCCACGGGAACACAGTCCTCTTATCCA 967
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/Jb bp mRNA linear EST 14-AUG-2002 QGB11N07.yg.abl QG_ABCD1 lettuce salinas Lactuca sativa cDNA clone QGB11N07, mRNA sequence.
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                                                                                                                                                                                                                                                                                               GlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGlyThr 181
                                                                                                                                                                                                                                                                                                                                 GluPheGluAlaValValGly---LysCysLysThrGluGluGluILeValGluArgGly 216
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                                                                                                                                                                                                                                                                                                                                                                                                                            182 AspPhe------GluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSer 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 LeuAlaAlaGlyAsnSerLeuGluGluAlaCySPhePheAlaAsnAlaAlaAlaGlyVal
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Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: &kozik@atgc.org [Michelmore@vegmail.ucdavis.edu]
572
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                                                                                                  Mismatches:
Indels:
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                                                                                                                                                                              from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. CDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
contig QG_CA_Contig5995, see http://cgpdb.ucdavis.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 rLysargLeuLysGlyAspSerArgProValasnProLeuGluGlnArgMetIleValLe
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                                                                                                            /db.xref="taxon:4236"
/clone="QGB11N07"
/clone_lib="QG_ABCDI lettuce salinas"
/lab_host="E.coli"
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62
27
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48
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MatcKes:
Conservative:
Mismatches:
Indels:
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TAG_SEQ=TCTGTGCGGG"
147 c 197 g 197 t
                                                                                 /organism="Lactuca sativa"/cultivar="Salinas"
                               Bll row: N column: 07.
Location/Qualifiers
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/clone_lib="PyBS"
/clone_lib="PyBS"
/dev_stage="Assexual blood stages"
/dev_stage="Assexual blood stages"
/dev_stage="Bc. coli %1-1 Blue"
/lab_host="E. coli %1-1 Blue"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/CB47 mice infected with Py1XL parasites, and leukcoytes removed by passage over microcrystalline cellulose collumns. Total RNA was isolated using the giannidinium isothicoyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XNOI and separated on a Sephacryl 5-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."
                                                                                                                              BM169900 629 bp mRNA linear EST 04-DEC-2001
EST572423 PyBS Plasmodium yoelii yoelii CDMA clone PYCPY36 5' end,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: carlton@tigr.org

Tor clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
                                                                                                                                                                                                                                                                                                                                                                                               Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
Fraser,C.M. and Carucci,D.J.
Plasmodium yoelli EST project at TIGR
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Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        usa
                        535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Jane Cariton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850,
Tel: 301-530-9319
Fax: 301-838-0208
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CAAACGAACAGAAGGAGTCTCAAGCACAGACATTGTTGGGAGGATG
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/db_xref="taxon:73239"
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FEATURES Location/Qualifiers 1. 689 /Organism="Physcomitrella patens subsp. patens" /Ob_xref="taxon:145481" /clone="pph3121" /clone=lb="full length CDNA library, chloronemata and young gametophores mixture of chloronemata and young gametophores with 2 to 5 leaves" BASE COUNT 176 a 185 c 143 g 184 t 1 others	Alignment Scores: 8.56e-09 Length: 689 Score: 167.50 Matches: 46 Score: 47.26% Conservative: 23 Percent Similarity: 31.51% Mismatches: 7 Query Match: 13 Gaps: 2	020-325 (1-477) x BJ165221 (1-689) GlaleualaargLysalaGlyValProValLeuIleAspProLysGlyThrAsp :::::	550 ATTCCAGAAGAACTTCTGAAATGTCTTACAGTGTTAAGTCCTAATGAGACGGAGCTGGCC 491 201 AlaValValGlyLySCySLySThrGluGluGluIleValGluArgGlyMetLySLeuIle 220 311 ::: 490 CGGCTAACTGATATGCCAACTATCAGGAGAAATTTTGAGGGCAGCTAAGAAGGTT 431 221 AlaAspTyrGluLeuSerAlaLeuLeuValThrArgSecIluGluGlyMetSerLeuLeu 240 311 ::::::::::::::::::::::::::::::::::		T 12
FEATI BASE ORIG	Alignm Pred. Score: Percen Best L Query DB:	Oy Oy Oy		6 6 6 6 6 6	RESUL B1944 B1944 LOCUS DEFIN VERSI SEYWO SOUG ORG
Oy 317 AspThrGlyPheGlyValMetThrGluGluGluLeuLysLeuAlaValAlaAlaAla 335 149 AATAAAAATAAAGGCTATATGGAGTTCAAAATTTTTTTTT	Qy 376 SerAspalaSerThrLysArgLeuLysGlyAspSerArgProValAsnProLeuGluGln 395 :::::: :::	409 ValValSerPheGluGluAspThrProGlnArgLeuIleAlaGlyIleLeuProAspLeu	OY 437 ProGludLulleAlaGlySerLysoluvaTrpAlaAsnGlyGluValLeuVal 455	BJ165221/C BJ165221 bJ165221 b 689 bp mRNA linear EST 24-JAN-2002 LOCUS BJ165221 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone pph3i21 a/, mRA sequence. BJ165221 GI:18333207 KEYWORDS EST. ORGANISM Physcomitrella patens subsp.:patens. ORGANISM Physcomitrella patens subsp. patens BYODED Physcomitrella BYODED PHYSCOMITRELIA BYODED PHYSCOM	TITLE Comparison of the moss Physcomitrella patens genome with flowering plants genome JOURNAL Unpublished (2002) Contact: Tadasu Shin-i Contact: Tadasus Shin-i Contact: Tadasus Shin-i Contact: Tadasus Shin-i Contact Shin-i Contact Tadasus Shin-i Contact Shin-i Contact Tadasus Shin-i Contact Tada

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254 GlnGluValTyrAspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThr 273
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AUTHORS
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BQ995975
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The library was prepared using the Stratagene pBluescript II SK(+) library construction Kit: Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. Tissue culture and library construction were performed by Francoise Thibad-Nissen and Anu Khana (Lila VodKin lab, University of Illinois)."
                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="differentiating somatic embryos cultered on MSM6AC"
'Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 GlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGlyThr 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 GATGGGCCCCTTCCACCACAATTATTGAATTTTGTTGATATTCTGAGTCCTAATGAAACT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 GluPheGluAlaValValGly---LysCysLysThrGluGluGluIleValGluArgGly 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 TTGAAATGC-----CATGAATTGGGAGTTAAGCAAGTTCTTGTGAAACTTGGGGAA 314
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                                                                                                                                                                            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 AspPhe-----GluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSer
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                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1075-538"
//clone_lib="Gm-c1075"
                                                                                        Unpublished (1999)
Context: Showmaker K/Public Soybean EST Project
Dublic Soybean EST Project
Washington University School of Medicine
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/note="Vector: pBRCDNASfiAB; The library was constructed from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB=0G_EFGHJ lettuce serriola TAG_LIB=0G_EFGHJ lettuce serriola TAG_LIB=0G_EFGHJ lettuce serriola 174G_SEC=TGFRACCGGG 162 t 8 others
                                                                                                                                                      EUSYSSY/S 686 bp mRNA linear EST 21-AUG-2002 QGG11110.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone QGG11110, mRNA sequence.
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Kozik, A., Michelmore, R. W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Daume, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison
Lin, H., van Daume, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositive Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                  Lactuca sativa
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraccae; Lactuceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Famil: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig5995, see http://cgpdb.ucdavis.edu/
for details.
274 LeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAla 290
                                                            435 TIGGITGAGGGCAAGICCAAAAAGGAATGCCTCAGATTTGCTGCTGCTGCG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="QGG11110"
/clone_lib="QG_EFGHJ lettuce serriola"
/lab_host="E.coli"
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58
34
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Indels:
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Matches:
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6.77%
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                     No.:
                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
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BF642033
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Grusak, M.A., Sanac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.
ESTS from developing reproductive tissues of Medicago truncatula Unpublished (2001)
Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
Fax: 713-798-7078
                                                                                                                                              243
                                                                                                                                                                                                       303
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                                                                                                                                                                                                                                                GCCCT-----CCGGTTACCCCTCTTCATGAAAGGATGATTATATGGTGAGTGCTGTGAAA 417
                                                                                                                                                                                                                                                                                                                                                 405 AlaValAspTrpValVal------SerPheGluGluAspThrProGlnArg 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 uIleAlaGlySerLysGluValTrpAla-----AsnGlyGlyGluValLeuValLe 456
                                                         324
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                                                                                                                                                                                                                                                                                       385 GlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeuGlyAlaLeuGlu 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591
                           76 AAGATGGGTTCGGATACA------GGTCTAGAGAACTCGAAGCGGTTTCCNNCG 123
                                                                                   124 ACATGGTTGATCGGAGGTTTGGTGGCAGGCTATCGGTTATGGGGTTATGCGCTGCTTGG 183
                                                                                                              325 GluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysValValMet 344
                                                                                                                                                                                         CCGGAGCTCTCCCCTCTGAGTATTGTTGGGAGGAAGAAGAAGAGGCCCATTCGTGTATAC
                                                                                                                                                                        LysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThrLysArgLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR sequence name: MTOAD46TK
More information is available at: www.medicago.org
seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
1. 729
 LysLeuGlyThrSerThrValSerProlleGluLeuGluAsnAlaValArg
                                                         -------GlyArgAlaAspThrGlyPheGlyValMet------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uAsnPheGluAspGlyCysSerThrThrAsnIleIleLysLysIle 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAACGAACAGAAGGAGTCTCAAGCACAGACATTGTTGGGAGGATG 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mgrusak@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI308004
BI308004.1 GI:14982331
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JOURNAL
COMMENT
297
                                                        314
                                                                                                                                             184
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KEYWORDS
SOURCE
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NF014A09INIF1068 Insect herbivory Medicago truncatula cDNA clone NF014A09INI 5', mRNA sequence.
BF642033.1 GI:11906191
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 GITGITAGIGAIGAIGAAAITATIGCIAAIAAGGGICCI-----CCIGITACCCCITIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 ArgLysArgGlyGluLysVal-----ValMetThrAsnGlyValPheAspIleLeuHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 AlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeuIleValAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SerPheGluGluAspThrProGlnArgLeuIleAlaGlyIleLeuProAspLeu
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46
31
55
55
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Mismatches:
Indels:
/organism="Medicago truncatula"
/cultivar="A17"
                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (1-729)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                   /cultivar="A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-912-020-325 (1-477) x BI308004
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158.00
52.74%
31.51%
6.60%
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KEYWORDS
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Location/Qualifiers

1. 609

(Apple 109)

/ Organism="Medicago truncatula"

/ Ab_xref="taxon:3880"

/ Clone="NF014A091N"

/ Clone="NF014A001N"

/ Clone="N
                                                                                                                                                                                                                  1 (bases 1 to 609)

Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J. and May, G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library

Unpublished (2000)
                                    Medicago truncatula
Rukaryota, Viridipliantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 GluGlnArgMetIleValLeuGlyAlaLeuGluAlaValAspTrpValVal----- 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....SerPheGluGluAspThrProGlnArgLeuIleAlaGlyIleLeuProAspLeu 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Korth K

Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
Fax: 501 575 7600.
Email: Kkorth@comp.uark.edu
Insert Length: 609 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Seg primer: TCACACAGGAAACAGCTATGAC
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                              REFERENCE
AUTHORS
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COMMENT
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SOURCE
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Db 455 CATGCCAAAAAGGCTGCCCTATAAACAGATTAAGCGCACGGAACGACTTCCAGCACT 514

Qy 466 Asnileile 468
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Db 515 GATATTGTG 523
Search completed: November 26, 2002, 22:39:52
Job time: 2410 secs
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2746, Ap 1, Appli 7, Appli 1, Appli 5, Appli 43, Appli

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APPLICANT: Mathan Dr., Michael J.
APPLICANT: Antan Dr., Christopher P.
APPLICANT: Conner Mr., Christopher P.
APPLICANT: Hiethoff Mr., Douglas M.
TITLE OF INVENTION: METHOD AND PROBES FOR THE IDENTIFICATION
TITLE OF INVENTION: OF MICROBIAL GENES SPECIFICALLY INDUCED DURING HOST
TITLE OF INVENTION: INFECTION
NUMBER OF SEQUENCES: 255
CORRESPONDENCE ADDRESS:
                                                                                                 Sequence 1, Al
Sequence 5, Al
Sequence 43, A
                                                                                                                                                                                                                                                     Sequence 6, P Sequence 6, P Sequence 6, P Sequence 6, P Sequence 4, P Sequence 6, P Sequence 6, P Sequence 3, P Sequence 13, P Sequence 16, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 16,
Sequence 7, P
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Seguence 1,
                                                                                                                                                                              Sequence 43
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Sequence (
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US-09-199-637A-1
US-09-194-0011-2746
US-08-826-611-1
US-08-840-198-1
US-08-840-198-1
US-08-841-198-1
US-08-108-115-43
US-09-265-315-43
US-09-265-315-43
US-09-265-315-43
US-09-265-315-43
US-09-265-315-43
US-09-265-315-43
US-08-76-233A-1
US-08-75-646A-6
US-08-75-646A-7
US-08-75-65-614-9
US-08-75-65-614-9
US-08-75-957A-4
US-08-95-957A-4
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,155B ,
FILING DATE: 17 -MAX-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  risman, Bynum & Johnson,
Fifteenth Street
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NAME: Petersen Mr., Steven C.
REGISTRATION NUMBER: 36,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/446-1300
TELEFAX: 303/449-5426
TELEX: ABA1475
                      3: Chrisman,
1900 Fifteent
    CITY: Boulder STATE: CO
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-Q-Cqqn2_1/YGPFO_spool/XG9912020/runat_25112002_091429_24273/app_query.fasta_1.647
-Q-Cqqn2_1/YGPFO_spool/XG9912020/runat_25112002_091429_24273/app_query.fasta_1.647
-Q-Cqqn2_1/YGPFO_spool/XG99912020_YGPFIX=p2n.rni -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS=human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCOREE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-WODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIXE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US09912020_GCGN_11_38_grunat_25112002_091429_24273 -NCPU-6 -ICPU-3
-NOA_XLPXY -NO_MANP -LARGEOURRY -NCG_SCORES-0 -WAIT -LONGLOG -DEV_TIMBOUT-120
-WARN TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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19, Appl
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19, Appl
2723, Ap
                                                                                                                               November 26, 2002, 10:27:12; Search time 73 Seconds (without alignments) 2003.902 Million cell updates/sec
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Sequence 2
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1 MKVFLPEFERAGVMVVGDVM......FEDGCSTINIIKKIQQDKKG
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                      GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                   nucleic search, using frame_plus_p2n model
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US-08-651-155B-186
US-08-134-001C-1684
US-08-920-812-19
US-08-920-827-19
US-08-920-828-19
US-08-134-001C-2723
US-09-134-001C-2723
US-09-139-637A-280
US-09-199-637A-272
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Scoring table:

Total number

Searched:

Minimum DB Maximum DB

Perfect score:

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Patent No. 6365401
GENERAL INFORMATION:
APPLICANT: Mahan Dr., Michael J.
APPLICANT: Gonner Mr., Christopher P.
APPLICANT: Hiethoff Mr., Douglas M.
TITLE OF INVENTION: METHOD AND PROBES FOR THE IDENTIFICATION
TITLE OF INVENTION: INFECTION
TITLE OF INVENTION: INFECTION
WUMBER OF SEQUENCES: 255
CORRESPONDENCE ADDRESS:
ADDRESSE: Chrisman, Bynum & Johnson, P.C.
STREET: 1900 Fifteenth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 HisprothrileThrLysLeuArgValLeuSer-ArgAsnGlnGlnLeulleArgLeuAs 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 CATCCGACGATTACCAAAACTGCGAGTACTACTACGTAATCAGGAGCTCATTGTGA- 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 SerLeuGlyAlaAsnAlaArgLeuValGlyLeuThrGly-IleAspAspAlaAla-ArgA 81
                                                                                                                                                                                                                                                                                                                                                                                                  42 LysValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAla
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Mismatches:
Indels:
                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,155B
FILLING DATE: 17-MAY-1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                 411.50
88.14%
83.90%
17.20%
                                   LENGTH: 347 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-08-651-155B-186
                                                                                                                                                                      US-08-651-155B-185
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                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                      ANTI-SENSE:
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GENERAL INFORMATION:
APPLICANT: LYAN DOUGETLE-Stamm et al
APPLICANT: LYAN DOUGETLE-STAMM et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267 IleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePhe 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 GAGTTGAGACAGGCCGTCGCCAGCGCGTAAGTC----GCGAGAAGTGTCATGACCAAC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ATCGGCGTGCTGGCGCGCGACCTG-GCCGCGGGAAATACCCTGGAAGAGGGGTGTTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327 GluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysValValMetThrAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 GlyValPheAspIle---LeuHis-----AlaGlyHisValSerTyrLeu 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 ---GCGTTCGATATCTGACGCCATTATGACGCAACTGGACCTATCGGATACTTA 281
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Staphylococcus epidermidis
               NAME: Petersen Mr., Steven C.
REGISTRATION NUMBER: 36,238
REBERENCE/DOCKET NUMBER: 17060.1
TELECOMUNICATION INFORMATION:
TELEPHONE: 303/546-1300
                                                                                                                       TELEFAX: 303/449-5426
TELEX: ABA1475
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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263.00
79.598
73.478
10.998
ATTORNEY/AGENT INFORMATION:
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SEQ ID NO 1684
LENGTH: 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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Score			165.50	Mat ches.	. 77	
Percent Sim Best Local Query Match DB:	nt S. Loca Mato	Percent Similarity: Best Local Similarity: Query Match: DB:	39.128 22.658 6.928	ative: hes:	5, 142 65 13	
0S-09	-912	-020-325 (1-4	77) x US-09-134-0	-001C-1684 (1-948	8).	
Oy Dp	2 7	•	roGluPheGluArgAl TGAAATGAATAAAAA	aGlyvalMetvalva ::: :: TAAAGTGATTGTAAT	LysvalThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMetLeu	21 66
γ̈́	22	,	yrGlyProThrSerAr	glleSerProGluAl		41
qq	29	GATAAA	-	AAGGTTTCCAAAA	AATGTTAAAAGGTTTCCAAAACCCGGTGAGACATTA 1	114
Š Š	42		SValAsnThrIleGluGluArgProGlyGly::::	yGlyAlaAl	LysValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsn 5	59
3 6	CTT S		CICAAAAGGAGIIIGG			
ر م م	175	_	IyAlaAsnAlaArgLe ::: CAGCAGATACAACATT	uValGlyLeuThrGl ::: TATCAGTAAAGTTGG	ILOALASSETLEUGLYALAASANALAAKGLEUVALGLYLEUTRIGIVILEASPARPALAALA 7 	79 234
0y	80		ysSerLeuAlaAspVa	lAsnValLysCysAs	ValSerValPro	66
qq	235	::: :: AACTTTATATTGGAA	: : AA	 	 -GATTTCAAAAAGCAGGT 2	267
ογ	100		leThrLysLeuArgVa	lLeuSerArgAsnGl	ThrHisProThrIleThrLysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeu	119
qq	268	ATTCAT	1 1 1 1 1	 ACACA	-ACACAATATATTTAACTTCA 2	294
ογ	120	AspPhe	GlyPheGl	GlyPheGluGlyValAspProGlnPro-	1	132
qq	295		CTGGGCAAGCATTTAT	CACTGTTGATGAAGC	:::	354
οy	133	;	-LeuHisGluArgIleAsnGlnAlaLeuSer	LeuSer	SerileGly 1	145
qq	355		GTGCGAATATGACATT	AAGTGCAACTGATGT	TGGAT	414
δ	146		AlaLeuValLeuSerAspTyrAlaLysGlyAlaLeu	yAlaLeu		161
q	415		:: :: CAGACTTTGTTGTAGC	GCAGCTTGAAGTTCC		474
οy	162		euAlaArgLysAlaGl	yValProValLeuIl	GlnMetIleGlnLeuAlaArgLySAlaGlyValProValLeuIleAspPro 1	178
qq	475		TTGCTCGTAAACAAA	TATCACTACTGTATT		534
οy	179			YThrAspPheGluAr	LysGlyThrAspPheGluArgTyrArgGlyAlaThr]	190
qq	535		ATTGAATTGCCTAAGTCACTTTTAGAGTTAACTGAT			570
ογ	191		snLeuSerGluPheGl	uAlaValValGlyLy		210
QQ	571		II :::III ACGAAACGGAAGCAGA	::: ATTATTAACAGGTAT		630
δ	211		rgGlyMetLysLeuIl	eAlaAspTyrGluLe		230
qq	631		AAACAGCAACATATTT	TCTCGATTTAGGTAT		069
ογ	231		lnGlyMetSerLeuLe	uGlnProGlyLysAl		250
pp	691		 AAGGCACGTATTGTGC	::: ATATCAAGAACAATA		747
Οý	251	-	luValTyrAspValTh	rGlyAlaGlyAspTh	ValileGlyValLeu	270
qq	748		AAGCAATAGATACGACA	AGCAGCAGGAGATACA	TTTATAGGTGCTTTT	807
δγ	271	AlaAlaThrLeuAlaAlaGly	-	-AsnSerLeuGluGluAlaCysPhePheAlaAsnAl	ø	289
qq	808		::::: ATAAAGATTTGAGCAA	::: AATTTAGAATCGGCTAT	::: TTAAGTGAGTTAAATAAAGATTTGAGCAATTTAGAATCGGCTATTCGACTTGCAAATCAA 8	867
ογ	290		alValGlyLysLeuGl	yThrSerThrValSe	AlaAlaGlyValValValGlyLySLeuGlyThrSerThrValSerProIleGluLeuGlu	309

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2024 ATCCCGAATATGCAAAACGCAGCCACGTTGTTCTTGGCACCATTAATGCTGACCAC 2083
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43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 TyrTrpTyrGlyProThrSerArglleSerProGluAlaProValProValValLysVal
                                                                                                                                                                                                                            Probe for Diagnosing Infectious Disease
                                                                                                                                                                                                                                                                                 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.2:
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/920,812
FILING DATE: 29-AUG-1997
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                       STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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PULDASJELZATON DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTONEY/AGENT INFORMATION:
NAME: Rib-Laures, Li-Helen
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                       Sequence 19, Application US/08920812 Patent No. 5763188 GENERAL INFORMATION:
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STRAIN: Clinical Isolate EC-39
                                                                                                                                             APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Gehas, Hirotsugu
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 19
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INFORMATION FOR SEQ ID NO: 19:
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151.00
39.62%
24.84%
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nucleic acid
EDNESS: double
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312/474-0448
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                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinoi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                    RESULT 4
US-08-920-812-19
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2132 ACCACTATCAGGTTGCATTT-GGCGGCAAAGGCGCGAATCAGGCTGTGGCTGCTGGGGGGT 2190
                                                                            2191 AGCGGTGCGAATATCGCGTTTATTGCCTGTACGGGTGATGACAGCATTGGTGAGAGCGTT 2250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAACTATCGTTCGCTTAACCCGCTCCGCCTCGCGAACTTCCTGACGAACTCTGCGCTG 2568
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2278 GATATTACTCCGGTCAGCGTATCAAGGCGAATCAACAGGTGTGGCGCTGATTTTTGTT 2337
                                                                                                                                                                                                                                                                                                                                                                                                                        2395 CCGGCGCTGGTGGAAGCGCAACGTGAGCGTATTGCCAACGCGTCAGCATTATTAATGAG 2454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2629 ATGATGAAGATGCAGCGAAGGCGGCGCAGGTACTTCATGAAAAAGGTATCCGTACTGTAC 2688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2689 TGATTACTITAGGAAGTCGTGTGTATGGGCTAGCGTGAATGGTGAAGGTCAG---CGCG 2745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2746 TICCIGGATICCGGGIGCAGGCIGICGATACCATIGCIGCCGGAGATACCTITAACGGIG 2805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 SerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThrHisPro 102
                                                                                                                                                                                                                 103 ThrileThrLysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAspPheGlu 122
                                                                                                                                                                                                                                                                                                     123 GluGlyPheGluGlyValAspProGlnProLeuHisGluArgIleAsnGlnAlaLeuSer 142
                                                                                                                                                                                                                                                                                                                                                                                             -----SerIleGlyAlaLeuValLeuSer 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           aGlyValProValLeuIleAspProLysGlyThr-AspPhe---GluArgTyrArgGlyA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euValThrArgSerGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisM 249
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                                      63 LeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeu
                                                                                                                                                                                                                                                                                                                                  209 luGluGluIleValGluArgClyMetLysLeuIleAlaAspTyrGluLeuSerAlaLeuL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 laThrLeuLeuThrProAsnLeuSerGluPheGluAlaValValGlyLySCysLysThrG
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APPLICANT: Matsuhisa, Akio
APPLICANT: Matsuhisa, Akio
APPLICANT: Eda, Soji
TTTLE OF INVENTION: Probe for Diagnosing Infectious Disea
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                       2251 CGCCAGCAGCTCGCCACTGATAACATT-----
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X: United States of America
60606-6402
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Patent No. 5770375
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COMPUTER READABLE FORM:
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US-08-920-827-19
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2024 ATCCCGAATATGCAAAACGCAGCCAGCCTCGTTGTTCTTGGCAGCATTAATGCTGACCAC 2083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2084 ATT-------CTTAATCTTCAATCTTTTCCTACTCCAGGCGAAACGTAACCGGTA 2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2278 GATATTACTCCGGTCAGCGTGATCAAAGGCGAATCAACAGGTGTGGCGCTGATTTTTGTT 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThrHisPro 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrIleThrLysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAspPheGlu 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GluGlyPheGluGlyValAspProGlnProLeuHisGluArglleAsnGlnAlaLeuSer 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 AsnThrIleGluGluArgProGlyGly---AlaAlaAsnValAlaMetAsnIleAlaSer 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 LeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeu 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3796
79
47
156
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                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-912-020-325 (1-477) x US-08-920-827-19 (1-3796)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
Indels:
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Matches:
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                                                                                                                                            PRIOR APPLICATION DARA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                       APPLICATION NUMBER: US/08/920,827
FILING DATE: 29-AUG-1997
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Escherichia coli
STRAIN: Clinical Isolate EC-39
                                                                                                                                                                                                                   NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1
TELECOMMUNICATION INFORMATION
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                            TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SO ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                   : 3796 base pairs
nucleic acid
EDNESS: double
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39.62%
24.84%
6.31%
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                                                                                                              FILING DATE: 29
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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MOLECULE TYPE: G
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic
STRANDEDNESS:
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                                                                                                       -----CTGGAATCACCACTCGAAAGTGTGATGGCAGCGGCGAAAATCGCCCATCAAAAT 2508
151 AspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArg-LysAl 170
                                                                                                                                                                                                                                                                                                                                                                                                          etProThrGlnAlaGlnGluValTyrAspValThrGlyAlaGlyAspThrValIleGlyV 269
                                                                              170 aGlyValProValLeuIleAspProLysGlyThr-AspPhe---GluArgTyrArgGlyA
                                                                                                                                                                                      2569 TGGACATTATTACGCCAAACGAAACGGAAGCAGAAAACTCGCGTATTCGTGTTGAAA
                                                                                                                                                            189 laThrLeuLeuThrProAsnLeuSerGluPheGluAlaValValGlyLysCysLysThrG
                                                                                                                                                                                                                                           209 luGluGluIleValGluArgGlyMetLysLeuIleAlaAspTyrGluLeuSerAlaLeuL
                                                                                                                                                                                                                                                                                                                         euValThrArgSerGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||||||||| ::: ||| ::: ||| CTGCCGCTGCGATTGCCGTAACGCTAAAGGCGCACAACCTTCCGTACG 2915
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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COUNTRY: United States of America,
ZIP: 60606-6402
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/921,177 FILING DATE: 29-AUG-1997
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APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Eda, Soji
TILLE OF INVENTION: Probe for INUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 3796 base pairs
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2509 AAAAACTATCGTTAACCCGCTCCGGCTCGCGAACTTCCT3ACGAACTCTGCGCTG 2568
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Mismatches:
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                                                                                                                                 ORGANISM: Escherichia coli
; STRAIN: Clinical Isolate EC-39
US-08-921-177-19
                      STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                          151.00
39.62%
24.84%
nucleic acid
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Best Local Similarity:
Query Match:
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2191 AGCGGTGCGAATATCGCGTTTATTGCCTGTACGGGTGATGACAGCATTGGTGAGGGGTT 2250
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2629 ATGATGAAGATGCAGCGAGGCGCGCAGGTACTCATGAAAAAGGTATCCGTACTGTAC 2688
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--CTTAATCTTCAATCTTTCCTACTCCAGGCGAAACGTAACCGGTA 2131
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                                                                                                        2132 ACCACTATCAGGTTGCATTT-GGCGGCAAAGGCGCGAATCAGGCTGTGGCTGCTGGGGGGT
                                                                                                                                                                  LeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                2278 GATATTACTCCGGTCAGCGTGATCAAAGGCGAATCAACAGGTGTGGCGCTGATTTTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 GluGlyPheGluGlyValAspProGlnProLeuHisGluArgIleAsnGlnAlaLeuSer
                                                    44 AsnThrIleGluGluArgProGlyGly---AlaAlaAsnValAlaMetAsnIleAlaSer
                                                                                                                                                                                                                                                                                                                                  251 CGCCAGCAGCTCGCCACTGATAACATT
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Patent No. 5853998
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Matsuhisa, Akio
APPLICANT: Uchara, Hirotsugu
APPLICANT: Bcda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Dis
UNMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Bory
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 $ CITY: Chicago
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US-08-920-828-19
2084 ATT---
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                                                                                                           2806 CGTTAATCACGGCATTGCTGGAAGAAAACCATTGCCAGAGGCGATTCGTTTTGCCCATG 2865
                                                    269 alLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnA 289
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                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Ohno, Tsuneya
APPLICANT: Matsuhisa, Akio
APPLICANT: Eda, Soji
TITLE OF INVENTION: Probe for Diagnosing Infectious Disease
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                  laAlaAlaGlyValValValGlyLysLeuGlyThrSerThrValSerPro 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,577C
FILING DATE: 27-MAR-1995
CLASSIFICATION: 536
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Indels:
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Matches:
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COUNTRY: United States of America
2IP: 60606-6402
COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; STRAIN: Clinical Isolate EC-39
US-08-362-577C-19
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NAME: Rin-Laures, Li-Hslan
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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151.00
39.628
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Best Local Similarity:
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MOLECULE TYPE: G
ORIGINAL SOURCE:
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STATE: Illinoi
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STRANDEDNESS
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Matches:
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CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 2723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2723, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
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54.68%
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Best Local Similarity:
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                                                                                                                           SOFTWARE: Patentin Release #1.0, AVersion #1.25 CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                          33,547
ER: 19036/32420
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Illinois
XY: United States of America
60606-6402
                                                                                                                                                            APPLICATION NUMBER: US/08/920,828
FILING DATE: 29-AUG-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,577
FILING DATE: 27-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                         NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 190:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 3796 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Escherichia coli
STRAIN: Clinical Isolate E
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151.00
39.62%
24.84%
6.31%
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                   CLASSIFICATION:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: WOLLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC FITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                1569 TGGACATTATTACGCCAAACGAAAGCAAAGCAAAAGCTCACCGGTATTCGTGTTGAAA 2628
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2395 CCGGCGCTGGFGGAAGCGCAACGTGAGCGTATTGCCAACGCGTCAGCATTATTAATGCAG 2454
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DD 79 AGAAGAGCTO OY 381 LysArgLeul DD 136 AACCAATCO OY 401 GlyAlaLeuc 1:::: DD 136 AACAATCTTT DD 136 ACCTAATT OY 421Ile DD 304 OY 459 Glullealac OY 459 Glullealac OY 459 GLULLEAC OY 459 GLULLEAC OY 459 GLULLEAC OY 636572 CORRESPOND CORRESPO	TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 149:	LENGTH 12804 TYPE: nucleic acid STRANDEDNESS: double	FORMATION FOR SEQ 1D NO: 149: SEQUENCE CHARACTERISTICS: TENGTH: 1796	TELEFHUNE: (000) 231-3000 TELEFAX: (608) 251-9166	TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:	REGISTRATION NUMBER: 27386	ATTORNEY/AGENT INFORMATION: NAME: Seay, Nicholas J.	APPLICATION NUMBER: 60/110,955 FILING DATE: 04-DEC-1998	PRIOR APPLICATION DATA:	FILING DATE: 03-Dec-1999 CLASSIFICATION: <unknown></unknown>	APPLICATION NUMBER: US/09/453,702B	SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA:	COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS	h. 1.44Mb	COUNTRY: US ZIP: 53701-2113	CITY: Madison . STATE: WI	ADDRESSEE: Quaries & Brady STREET: 1 South Pinckney Street	NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS:	Sequences of E. coli	Perna, Nicole T. Plunkett, Guy	, Fre	Patent No. 6365723 GENERAL INFORMATION:	KESULT 10 US-09-453-702B-149/c Sequence 149, Application US/09453702B	ATCTCAACTACCAAAATCAAGCAAGAATTATACGA	CysSerThrThrAsnIleIleLysLysIleGlnGlnAspLysLysGly	139 GlulleAlaGlvSerLvsGluValTrpAlaAsnGlvGlvGluValLeuValTeuAsnPh	AAAGA		136 AACCAAATCAAAAACAAAAATCATATTATGATTATGAACAACGTAAGATGTT	381 LysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeu :::::: :::::	

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QY Pb	31	ArgileSerProG	roGluAlaProValProValValLysVal ::: 	alValLysValAsnThrI ::::: TACTGCCTTGT	rlleGluGluArgPro	50
	α	GlyGlyAlaA.	laAsnValAlaMetAs 	. 5 – F	ים פו	69 9768
k &	7	ValGlyLeuThrGlyIl	GlyLeuThrGlyIleAspAspAlaAlaArg	laArgAlaLeuSerLy		. 6
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Dp	9707	GGAGTCGATATCA	CGTATCTGAAGCAAG!	ATGAATGGCACCGGAC	ATCCACGGTGCTT	9651
Qy Db	109 9650	ValLeuSerArgA::: GTCGATCTGA	euSerArgAsnGlnGln :: TCGATCTGAACGATCAAGGGGAACC	STTCATTTACGTTT	LeuIleArgLeuAspPhe :::::: ATGGTCCGCCCAGTGCC	121 9594
Oy Dp	122 9593	GluGluGlyPheG ::: GATCTTTTTTAG	GluGlyPheGluGlyValAsp 	 GČT	GGCGACATGGTAACATGGCGACATGGCAATGGTTACAT	135 9537
Oy Db	136	ArglleAsnGlnAl	aLeuSerSerlleG - -CTCTGTTCAATT-	1yA1 GC	aLeuValLeuSerAspTyrAlaLysGly GTIGTCTGCCGAGCCTTCGCGTACCAGC	155 9495
Οŷ	15	aLeuAlaSer	GlnMetIleG	lnLe	sAlaGlyValProValLeu	75
Dp	9494	GCATTTACTGCGA	GAGATC	CGGCATGO	CGGAGGTTTGTCAGC	9447
λο 4	17	leAspProLys	sGlyThrAsp		EBBCECECCCCEC	
g ;	4 (GATCCCAR	TICGIGAGGICIAI	GGCAAGACGAGCAIII	TILDIO	מ מ
ΟΥ Db	183 9386	PheGluArgTyrA: ::: CGGCAGGCGCTAC	fTyrArgGlyAlaThrLeuLe ::: ::TACAACTGGCGGATGTCG	rargGlyAlaThrLeuLeuThrProAsnLeuSərGLuPheGLi ::: :::: ACAACTGGCGGATGTCGTCAGCTCTCGGAAGAAGAATGGCG	rGluPheGluAlaVal :: AGNATGGCGACTTATC	202 9327
Oy Op	203 9326	ValGlyLysCysL AGTGGAAAAACAC	GlyLysCysLysThrGluGluGluIle GGAAAACACAGAACGATCGGGATATA	eValGluArgGly	MetLysLeuIleAlaAsp :::	222 9279
Qy Dp	223	TyrGluLeuSerA ::::: TATGAGATCGCCA	GluLeuSerAlaLeuLeuValThrArgSer :::::: AGATCGCCATGCTGTTGGTGACTAAAGGT	GluGlnGly. ::: GCAGAAGGG	GluGlnGlyMetSerLeuLeuGlnPro ::: :: GCAGAAGGGTGGTGGTCTGTTATCGA	242 9219
Qy Dp	243 9218	GlyLysAlaProLe ::: GACAAGTTCAC	euHisMetProThrGln CATTTTGCTGGAATG	AlaGlnGluVe ::: :rcrGrGGATTG	NTyraspvalThrGlyAla 	262 9162
Qy Db	263 9161	prhr TGCGTTC	ValileGlyValLeuAlaAlaThr ::: GTTGCCGGGTTACTCACAGGTCTG	LeuAl rccrc	.aAlaGlyAsnSerLeuGlu :: ::: :TACGGGATTATCTACAGAT	281 9102
Qy	282	Glu GAGAGAAATGC	AlaCysPhePl	AlaCysPhePheAlaAsnAlaAlaAlaGlyValValValValGl: AGAAATGCGAGGAATTATCGATCTCGCTCAACGTTGCGGAGGGCTTGCAGTAAC	aAlaGlyValValValGly ::: CGGAGCGCTTGCAGTAACG	296
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                                                                        GENERAL INCORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Adsubel, Frederick
APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Rahme, Laurence G.
APPLICANT: Tan, Man Wah
APPLICANT: Tsongalls, John
TILE OF INVENTION: SEQUENCES AND USES THEREOF
TILE FERENCE: 00786/36.1002
CURRENT APPLICANTON NUMBER: US/09/199,637A
FRICH APPLICANTON NUMBER: 1998-11-25
PRIOR FILLING DATE: 1998-11-25
PRIOR FILLING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SEQ ID NO 280
LENGTH. 2580
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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                       Sequence 280, Application US/09199637A Patent No. 6355411
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US-09-199-637A-280
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163 MetileGlnLeu-----AlaArgLysAlaGlyValProValLeuIleAspProLysGly 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnProLeuGluGlnArgMetIleValLeu.......GlyAlaLeuGluAlaVal
                                                                            AlaValValSlyLysCysLysThrGluGluGluIleValGluArqGlyMetLysLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585 ATCAACGCC3AAGTGCCGGACGGCCTCAAGGACAAGCGCCTGCTGGCCCTGGACATGGGG
                                                                                                                                                                                                                                                  181 ThrAspPheGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----CTGAAGGCGGTCCTC-----AACGAACTGGGCAAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       466 AsnileileLysLysileGlnGlnAspLysLys 476
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ΟŅ	181	ThraspPheGluargTyrArgGlyAlaThrLeuLeuThrPrcAsnLeuSer	197
qq	2322	GTC	2281
Qy	198	GlupheGlu	200
QΩ	2280	ATCAACGGCGAAGTGCCGGACGGCCTCAAGGACAAGCGCCTG&TGGCCCTGGAGGACATGGGG	2221
Qy dy	201	AlaValValGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle	220
3 8	2 6	3] vMet Sert.enT.e	4.0
qq	_		
Qy	241	ırG	260
QQ	2145	÷	2098
Oy	261	GlyvalLeuAlaAl	280
Op	2097	GGCGCCGGCAAGGCGGAAGGTGCCATGGACGCGCAACATGCTC	2053
Οy	281	GluGluAlaCysPhe-PheAlaAsnAlaAlaGlyValValValGlyLysLeuGlyTh	300
qq	2052	AAGCCGGCTCTGGCGCGCGCGGGGCTCGCTCGGTCGGTGCTACTACC	2002
Qy	300	rSerThr-ValSerProlleGluLeuGluAsnAlaValArgGlyArgAlaAspThrG	319
QQ	2004	CICGACGAGIAICGCCAGIACATCGAGAIGCCGCGCTGGAGGCCGCTTCCAGAAG	1945
Qy	319	lyPheGlyValMetThrGlu-GluGluLeuLysLeuAlaValÀlaAlaAlaArgLySArg	338
qq	1944	GICCTGGTGGACGAACGAGGAAGACACCATCGCATCCTCCGTGGCCTCAAGGAA	1885
Qy	339	GlyGluLysValValMetThrAsnGlyValPheAspIleLeuHisAla	354
qq	1884	CGCTATGAAGTGCACCACGGGTGAGCATCACCGACGGCGCATCATCGCCGCG	1831
ΟY	355	GlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeuIleVal	372
QC	1830	GCCAAGCTGTCGCACCGCTACATCACCGAT CGGCAACTGCCCGACAAGGCCATCGAC	1774
Qy	373	AlaValAsnSerAspAlaSerThrLysArgLeuLysGlyAspSerArgProVal	390
QQ	1773	CTGATCGACGAGCCGCAGCCGCATCCGCATGGAGATCGACTCTAAGCCGGAGGAACTG	1714
Οy	391	AsnProLeuGluGlnArgMetIleValLeuGlyAlaLeuGluAlaVal	406
qq	1713	GATCGTCTCGACCGTCGCTGATCCAGCTGAGATCGAGCGCGASSCGCTGAAGGAA	1654
δy	407	lValSerPheGluGluAspThrProGlnArgLeuIl@AlaGly	426
QQ	1653	GACGAAGCCACCAGGAAGCGCCTGGCCAAG	1615
Οy	427	yGlyAspTyrLysProGluGluIle	446
qq	1614	CTCGAGCGCGAATACGCCGACCTCGAGGAGAT	1567
δλ	447	uAsnPheGluAspGlyCys	465
qq	1566	THE THE THE TRANSPORTED THE TRANSPORT THE TR	1531
Oy	466	AsnilelleLysLyslleGlnGlnAspLysLys 476	
qq	1530	CAGATCCAGCAGAAGATCGAGCAGGCCAAGCAG 1	
RESI US-(ULT 13 09-221 equencatent	SULT 13 -09-221-017B-757 Sequence 757, Application US/09221017B Patent No. 6444799	

209

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1026 GGCCCTTANGCCGCTGACGCTTTTTGGGGGTCGGATATGGCTCTGCATTTCGATGGCATT 1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 AlaAspThrGlyPheGlyValMetThrGluGluGluLeuLysLeuAlaValAlaAlaAla 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336 ArgLysArg3lyGluLysValValMetThrAsnGlyValPheAspIleLeuHisAlaGly 355
       83 SerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThrHisPro 102
                                                                       ----CTGGTGACCATGCCGATCAACAAA 665
                                                                                                                                                                                                          666 GCAGCCATGCCGCAGGACATCTTTCCATACAAAGGCCATACGGAATACCTGCAGGCCCAA 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150 SerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArgLys 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 AlaGlyValProValLeuIleAspProLysGlyThrAspPheGluArgTyrArgGlyAla 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 Glu---------------GluIleValGluArgGlyMetLysLeuIle 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 AspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGly 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerAspAlaSerThrLysArgLeuLysGlyAspSerArgProValAsnProLeuGluGln 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            846 CTGGACAAGCTGAAGGCTTTCGATCGCAGCCTCCGCATGGATTTCGGTATAGTACGTCCG
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                                                                                                                                       103 ThrIleThrLysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAspPheGlu
                                                                                                                                                                                                                                                                                                                                                                                                             131 ---GlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIleGlyAlaLeuValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        190 ThrLeuLeuThrProAsnLeuSerGluPheGluAlaValValGlyLysCysLysThrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- GluLeuSerAlaLeu
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                                                                                                                                                                                                                                                                          123 GluGlyPheGluGlyValAspPro-----
                                                                       621 AAGCAAGCCGATGCGGATGTG-----
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APPLICANT: ROSS, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF NUMBER OF SEQUENCES: 1120
NUMBER OF SEQUENCES: ADDRESSS: ADDRESSSE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-912-020-325 (1-477) x US-09-221-017B-757 (1-3058)
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Conservative:
Mismatches:
Indels;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FASTSEO for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/AU98/01023 FILING DATE: 10-DEC-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2734
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
                                                                                                                                                                                                   CIT:.
STATE: CA
COUNTY: USA
ZIP: 9434-1018
COMPUTER READABLE FORM:
WEDIUM TYPE: Diskette
"TOP: IBM COMPATIBLE
"TOP: TEM COMPATIBLE
"TOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION UNBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 706141
INFORMATION FOR SEQ ID NO: 757:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
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35.018
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TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 1...3058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             circular
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                                                                                                                                                     STREET: 755 ....
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: UN
ORIGINAL SOURCE
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1641 GATCACCACGAGATCGTCAAGAAGCTGAATATAGAGGCTTTCGTAGTGGGGGACGACTGG 1700
                                                                                                                                                                                                                      1701 AAT-------GGCAAATACGACTATCTGAAGGATCTCGGCGTTCAGGTCTTT 1745
                                                                                                                                                                        LysProGluGluIleAlaGlySerLysGluValTrpAlaAsn --- GlyGlyGluValLeu 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 AlaAsnValAlaMetAsnIleAlaSerLeu-----GlyAlaAsnAlaArgLeuValGly 71
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                                                                                                                                                                                                                                                                       455 ValLeuAsnPheGluAspGlyCysSerThrThrAsnIleIleLysLysIle 471
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GENERAL INFORMATION:
APPLICANT: ANSUDE1, Frederick
APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Tan, Man-Wah
APPLICANT: Tanongalis, John
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
TITLE OF INVENTION UNMBER: US/09/199, 637A
CURRENT FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
SELENTH: AL235
THENTH: AL235
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Conservative:
Mismatches:
Indels:
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; LOCATION: (1)...(42235)
... OTHER INFORMATION: N is any nucleic acid.
US-09-199-637A-1
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138.50
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-09-199-637A-1/C
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Pred. No.:
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25669 AAGCGCGCCGAGGAAGGCAACTCGACCCGGTGATCGGTCGCGACGACGAGATCCGCCGG 25610
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                         25726 ---GACCCGAACGTCGAGGAGTCGCGCCCAGGCGCTGGACAAGTACACCGTCGACATGACC 25670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25231 CTCGACGAGTATCGCCAGTACATCGAGAAGGATGCCGCGCTGGAGCGCCCCCTTCCAGAAG 25172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                373 AlaValAsnSerAspAlaSerThrLysArgLeuLysGlyAspSerArgPro----Val 390
                                                                                                                                                     130 ProGlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIleGlyAlaLeuValLeu 149
                                                                                                                                                                                                                               SerAspTyrAlaLysGlyAlaLeu------AlaSerValGlnGln 162
                                                                                                                                                                                                                                                                                                        163 MetileGlnLeu-----AlaArgLysAlaGlyValProValLeuIleAspProLysGly 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221 AlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeu 240
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ValSerValProThrHisProThrIleThrLysLeuArgValLeuSerArgAsnGlnGln 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GluGluAlaCysPhe-PheAlaAsnAlaAlaAlaGlyValValValValGlyLysLeuGlyTh 300
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                                                                            ----GluGiyPheGluGlyValAsp
                                                                                                                                                                                                                                                                                                                                                                                 181 ThrAspPheGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeuSer-----
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694 GTTGATCAA------CATCAAAGCATTAAAGCTGTGAATCCACAAGGA 735
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                                          183 PheGluArg-----TyrArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPhe 199
                                                                                                                                                                                                                                                                                                                                                                                                                  275 AlaalaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaGlyValVal 294
                                                                                                                                      517 GTTGAAACAGTATTACCATATCGA---CCATTATTATTAAACCAAACAAAGATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                       LeulleAlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSer
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                                                                                                               GlualaValValGly---LysCysLysThrGluGluGluIleValGluArgGlyMetLys
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GEMERAL INFORMATION:
FAPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION:
FILE OF SEQ ID NOS: 5674

SEQ ID NO 2746

LENGTH: 939
24841 GAGGATATCGTCAAG------CTCGAGCGCGAATACGCCGACCTCGAGGAGATC 24794
                                                                                                                                                                     ----GGCTCGGCG 24758
                                                         427 AspLeuLeuValLysGlyGlyAspTyrLysProGluGluIleAlaGlySerLysGluVal 446
                                                                                                                                447 Trp---AlaAsnGlyGlyGluValLeuValLeuAsnPheGluAspGlyCysSerThrThr 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-912-020-325 (1-477) x US-09-134-001C-2746 (1-939)
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                               24757 CAGATCCAGCAGAAGATCGAGCAGGCCAAGCAG 24725
                                                                                                                                                                                                          466 AsnilelleLysLyslleGlnGlnAspLysLys 476
                                                                                                                                                                   24793 TGGAAGTCCGAGAAGGCCGAGGTGCAG-----
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Best Local Similarity:
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Scoring table:

Minimum DB Maximum DB

Searched:

Perfect score:

Sequence:

OM protein

Run on:

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Sequence 116, App
Sequence 6279, Ap
Sequence 1264, Ap
Sequence 210, App
Sequence 9242, Ap
7981, Ap
7757, Ap
6795, Ap
532, App
4, Appli
747, App
839, App
6938, Ap
                                                                                   747, App
839, App
839, App
286, App
6309, Ap
9785, Ap
6200, Ap
8205, Ap
8077, Ap
8019, App
8055, Ap
4137, Ap
8055, Ap
6057, App
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627, App
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Fetent No. US2002022718A1
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
FLIE REFERENCE:
CURRENT APPLICATION UNBER: US/09/741,669
CURRENT APPLICATION NUMBER: US 60/173005
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR PILING DATE: 1999-12-33
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FASTERQ for Windows Version 4:0
               US-09-815-242-7757

US-09-815-242-6795

US-09-070-927A-4

US-09-070-927A-4

US-09-974-300-747

US-09-974-300-839

US-09-815-242-6986

US-09-815-242-9866

US-09-815-242-9785

US-09-815-242-9785

US-09-815-242-9785

US-09-815-242-9785

US-09-815-242-9785

US-09-815-242-9919

US-09-915-341-16

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US-09-916-314-16

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US-09-914-314-16

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US-09-917-800A-1264
US-09-070-927A-210
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US-09-880-107-3376
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     TYPE: DNA ORGANISM: Escherichia coli
   SOFTWARE: Fast
SEQ ID NO 276
LENGTH: 1434
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-Q-\cgn2_1/USPTQ_spool/US09912020/runat_25112002_091430_24365/app_query.fasta_1.647
-Q-\cgn2_1/USPTQ_spool/US09912020/runat_25112002_091430_24365/app_query.fasta_1.647
-DEVEDLAD-APDIJACALONS_NA -QFMT-fastap -SUFFIX-P2n.rnpb -MINMATCH=0.1
-LOOPEXT-0 -LOOPEXT-0 -UNITS-blits -START-1 -END--1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -QUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USER-US09912020_0 -GGN_11_47_erunat_25112002_091430_24365
-NCPU-5 -NCPU-3 -NO_XLPXY -NO_MMAP -LAREQUERY -NG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS-1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 276, App
Sequence 165, App
Sequence 6204, Ap
Sequence 9661, Ap
                                                                                                              November 26, 2002, 22:04:38 ; Search time 113 Seconds (without alignments) 1625.664 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                    1 MKVTLPEFERAGVMVVGDVM......FEDGCSTTNIIKKIQQDKKG 477
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_MEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_MEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
10: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
11: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
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               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                   nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-741-669-276
US-09-912-020-165
US-09-815-242-6204
US-09-815-242-9661
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                             341543 seqs, 192557720 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                      Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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seq length: 2000000000
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Database :

2393 2393 2393 2265

Score

Ş. Result

100.004			CROULT C. RESOLT C. Sequence 165, Application US/09912020 Fatent No. US20020045592A1 GENERAL INFORMATION: APPLICANT: Zyskind, Judith APPLICANT: Zyskind, Judith APPLICANT: Trawick, John APPLICANT: Trawick, John APPLICANT: Forsyth, R. Allyn APPLICANT: Froelich, Jamle M. APPLICANT: Carr, Grant J. APPLICANT: Yamamoto, Robert T. APPLICANT: Yamamoto, Robert T. APPLICANT: W. H. Howard TTILE OF INVENTION: GENES IDENTIFIED A	TITLE OF INVENTION: ESCHERICHIA COLI CURRENT APPLICATION NUMBER: US/09/912, CURRENT FILING DATE: 2001-07-23 PRIOR APPLICATION NUMBER: 09/492,709 PRIOR FILING DATE: 2000-01-27 PRIOR PELLOR DATE: 1999-01-27 PRIOR PILING DATE: 1999-01-27 NUMBER OF SEQ ID NOS: 485 SOFTWARE: FESTSEQ for Windows Version SEQ ID NO 165 LENGTH: 1434 TYPE: DNA CREANISM: E. COLI	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Loc.008 Mi Query Match: DB: US-09-912-020-325 (1-477) x US-09-912-020 Qy 1 MetLysValThrLeuProGluPheGluArgA
Scool	Matches 1993.00 Matches 477	41 VallysvalAsnThrTleGluGluArgProGlyGlyAlaAlaAsnValAlaMecAsnIle	121 PheGluGluGluGluGlyValAspProGlnProLeuHisGluArglleAsnGlnAla	101 AlavalvalGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle 101 AlavalvalGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle 101 AlavalvalGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle 101 AlavalvalGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle 101 AlavalvalGluLeuSerAlaLeuLeuValThrargSerGluGlnGlyMetSerLeuLeu 101 AlaaspTyrGluLeuSerAlaLeuLeuValThrargSerGluGlnGlyMetSerLeuLeu 101 AlaaspTyrGluLeuSerAlaLeuLeuValThrargSerGluGlnGlyMetSerLeuLeu 101 AlaaspTyrGluLeuSerAlaLeuLeuValThrargSerGluGlnGlyMetSerLeuLeu 101 AlaaspTyrGluLeuSerAlaLeuLeuValThrargSerGluGlnGluGlyMetSerLeuLeu 101 AlaaspTyrGluLeuSerAlaProLeuLeuValThrargSerGluGluValTyraspValThr 101 AlaaspTyrGlySalaProLeuHisMetProThrGlnAlaGlnGluValTyraspValThr 101 AlaaspTyrGlyGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyraspValThr 101 AlaaspTyrGlyGlyLysAlaProCeAACGCAAGCGGAAGGGAATGGTTACGATACCAAGCGGAAGGAA	261 GlyAlaGlyAspThYalileGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu GlyAlaGlyAspThYalileGlyValLeuAlaAlaAhrLeuAlaAlaGlyAsnSerLeu

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DileLeuHisAlaGlyHisValSerTyrLeu 360
                                              JILEVALALAVALASNSERASPALASETTHR 380
                                                                        AsnProLeuGluGlnArgMetIleValLeu 400
                                                                                                 GCCGTAGCGGCAGCGCGTAAACGTGGTGAA 1020
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Matches:
Conservative: (
Mismatches: (
Indels: (
Gaps:
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             LysArgLeuLysGlyAspSerArgProValAsnProLeuGluGluGlnArgMetIleValLeu
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Matches:
Conservative:
Mismatches:
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: 1000-11.0
TITLE OF INVENTION: 1000-11.0
TITLE OF INVENTION: 1000-10.2
PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-16
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                            Sequence 6204, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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ORGANISM: Escherichia
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Best Local Similarity:
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US-09-815-242-6204
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LENGTH: 1434
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                     PheGluGluGlyPheGluGlyValAspProGlnProLeuHisGluArglleAsnGlnAla 140
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                                                                                                                  AlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeu
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ATGAAAGTAACGCTGCCAGAGTTTGAACGTGCAGGAGTGATGGTGGTGGTGATGTGATG
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oy D		MettysvalthrLeuproGluPheGluArgAlaGlyvalMetValValGlyAspvalMet 20 	_
oy Ob	21	LeuaspargTyrTrpTyrGlyProThrSerArgIleSerProGlualaProValProVal 40 	_
Qy Db	41	GlyalaalaasnValalametasnIle 6 	· -
Qy Dp	61	reuGlyalaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArg 8 	~ -
Qy Db	81	AlaLeuSerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThr 100 	
Oy Dp	101	HisProThrIleThrLysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAsp 120 	~ -
QY	121 361	PheGluGluGluGlyPheGluGlyValAspProGlnProLeuHisGluArgIleAsnGlnAla 140 	
Oy Dp	141	LeuserserileglyalaLeuvalLeuseraspTyralaLysGlyalaLeualaserval 160 	
Oy Db	161	GInGInMetIleGInLeuAlaArgLysAlaGIyValProValLeuIleAspProLysGly 180 	
Oy Db	181	ThraspPheGluargTyrargGlyalaThrLeuLeuThrProasnLeuSerGluPheGlu 200 	
Qy	201	AlaValValGlyLySCySLysThrGluGluGluIleValGluArgGlyMetLySLeuIle 220 	
Oy Dp	221	AlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeu 240 	
Qy	241	GInProGlyLysAlaProLeuHisMetProThrchaglnGluValTyrAspValThr 260 	
Qy Db	261	GlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu 280 	
oy Ob	281	GluGluAlaCysPhePheAlaAsnAlaAlaGlyValValValGlyLysLeuGlyThr 300 	
Oy Db	301	SerThrvalSerProIleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPhe 320 	
Qy Db	321	GlyValMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGlu 340 	
O.Y	341	LysValValMetThrasnGlyValPheaspIleLeuHisalaGlyHisValSerTyrLeu 360 	
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361 AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr 380
                                                                                          Length:
Matches:
Conservative::
Mismatches:
Indels:
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2265.00
97.48%
93.49%
                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(1434)
US-09-815-242-9661
                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                  US-09-815-242-9661
                                                                                                                                                                                                                                                                  SOFTWARE: Fast:
SEQ ID NO 9661
LENGTH: 1434
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                                                                                                                                                                                                                                                                                                    TTCGAGGAACCGTTCCGC---ACCGACGCGGCGCCCTGGCCGTGGACGTCGAGTCGCTG 417
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                                                                                                                                                                                                                                                                                                                                                                                             181 ThraspPheGluargTyrargGlyalaThrLeuLeuThrProAsnLeuSerGluPheGlu 200
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                                            US-09-912-020-325 (1-477) x US-09-815-242-7981 (1-1425)
 Conservative:
Mismatches:
Indels:
                             Gaps:
72.73%
57.93%
56.44%
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Percent Similarity:
Best Local Similarity:
                   Query Match
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958 GGCGTGCTGGGCCTGGAGCAATTGCTGGCAATCGAAGACGCCCGCGCCACGGCGAG 1017
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APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Brokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 05/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/205,57
PRIOR APPLICATION NUMBER: 60/205,57
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2001-12-22
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE FEATSED FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7757, Application US/09815242
Patent No. US20020061569A1
GENERAL INPORMATON:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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; LOCATION: (1)...(927)
US-09-815-242-7757
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LENGTH: 927
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5.67e-13 Length: 927 197.00 Matches: 86 126.448 Mismatches: 150 8.238 Mismatches: 150 8.238 Mismatches: 150 8.238 Indels: 150 10.00	Oy 312 ValargGl;ArgAla 316 :::	; Patent No. US20020061569A1 ; GENERAL INFORMATION: ; APPLICANT: Haselbeck, Rober ; APPLICANT: Ohlsen, Kari L. ; APPLICANT: Zyskind, Judith	; APPLICANT: Wall, Daniel ; APPLICANT: Travick, John D; ; APPLICANT: Carr, Grant J. ; APPLICANT: Yamamoto, Rober	; APPLICANT: Xu, H. Howard ; TITLE OF INVENTION: Identif; ; TITLE OF INVENTION: PECKART; ; FILE REFERENCE: ELITRA.011A	CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2001- PRIOR APPLICATION NUMBER: 6 PRIOR FILING DATE: 2000-03-	; PRIOR APPLICATION NUMBER: 6 ; PRIOR FILING DATE: 2000-05- ; PRIOR APPLICATION NUMBER: 6 ; PRIOR FILING DATE: 2000-05-	; PRIOR APPLICATION NUMBER: 6 ; PRIOR FILING DATE: 2000-10- ; PRIOR APPLICATION NUMBER: 6 ; PRIOR FILING DATE: 2000-11-	; PRIOR APPLICATION NUMBER: 6 ; PRIOR FILING DATE: 2000-12-; ; PRIOR APPLICATION NUMBER: 6 ; PRIOR FILING DATE: 2001-02-	; NUMBER OF SEQ ID NOS: 14110 ; SOFTWARE: FastSEQ for Window ; SEQ ID NO 6795 ; LENGTH: 918	; TYPE: DNA ; ORGANISM: Enterococcus faec ; FEATURE: ; NAME/KEY: CDS	LOCATION: (1)(918 9-815-242-6795 nment Scores:	Pred. No.: 2.29e Score: 1915.50 Percent Similarity: 42.728 Best Local Similarity: 22.788		Oy 13 ValMetValValGlyAspVa: ::::: :: Db 16 GTTACAATTATCGGAAGTAT	Qy 33 SerProGlualaProValPro	Qy 53AlaAlaAsnVa: Db 118 GGTGGTAAAGGAGCAAACCA	Oy 70 ValGlyLeuThrGlyLleAsp ::: Dh 178 ATTGGTGGTGTGGGAAATGA
5.67e-13 Matches: 197 00 Anismatches 8.23\$ Mismatches 8.23\$ Mismatches 10 47.7) x US-09-815-242-7757 (11metvalvalGlyAspvalMetLeuAs; 11 11 11 11 11 11 11 11	· · · · · · · · · · · · · · · · · · ·		ValLysValAsn 									AGCGCC					
		-477) x US-09-815-242-7757 (slmetValValGlyAspValMetLeuAs; ::: :: :: :: RCTGGTGGTGGCAGCCTGAACATGGA	SerArgIleSerProGluAlaProGCGCGCGCGCGCGCGCGCTT	luargPro61y61yAlaAlaAsnVa CCGGCGGCAAGGGAGCCAACCA	laargLeuValGlyLeuThrGlyIleAs; ::::: rGGCGATGATCGGCTGCTTGGCGACGA	laAspValAsnValLySCySAspPheVa ::: AGGCCGAGGGCATGCACTGCCAGGCGTv	ysLeuArgValLeuSerArgAsnGlnGl. cGCTGATCGTGGTCGACGACAGCAGCACCA	GluGlyPheGluGlyValAspProGlnProLeu	leGlyAlaLeuValLeuSerAspTyrAl 	leGinLeuAlaArgiysAlaGlyValPr ::::: rGGGCCGGGCCATGCGCTGGGCAGAC	lythraspPheGluargTyrargGlyal. acGTGCCGGCGGAGTGCTGCCGTGGT	/alGlyL	etLysteulleAlaAspTyrGluLeuSe ::: :: :: CCGAGCGCCTGCGCGAAATGGGCGCCGG	etSerLeuLeuGlnProGlyLysAlaPr ::: CCTGCTGGTAGGCGAGGGCGGGTCGA	yrAspValThrGlyAlaGlyAspThrVa 	1yAsnSerLeuGluGluAlaCysPhePh 	ysLeuGlyThrSerThrValSerProIl :: sccrcGGGGGGAGACCTCGATC

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1 AAA---GAAATGCCAAAACCAGGCGAAACAATTCACGCCATTGAACATTTTACAGCGGGT 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 GGTGGTAAAGGAGCAAACCAAGCAGTCGCAGCGAAACGTTCAGGCGCCAGAAACATATTT 177
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                                                                                                                                                                                                                                                                                                                                                                                                                    PELICANT: Travick, John D.
PELICANT: Travick, John D.
PELICANT: Travick, John D.
PELICANT: Carr, Grant J.
PELICANT: Xu, H. Howard
TILE OF INVENTION: Identification of Essential Genes in Tractic OF INVENTION: Identification of Essential Genes in Tract OF ILING DATE: 2001-03-21
TILE OF INVENTION NUMBER: 60/29/19/10/18
TILING DATE: 2000-05-23
TIOR APPLICATION NUMBER: 60/20/22/27
TIOR PELLING DATE: 2000-10-23
TIOR PELLING DATE: 2000-110-23
TIOR APPLICATION NUMBER: 60/253/625
TIOR APPLICATION NUMBER: 60/253/625
TIOR APPLICATION NUMBER: 60/253/931
TIOR PILING DATE: 2000-112-22
TIOR APPLICATION NUMBER: 60/253/931
TIOR PILING DATE: 2001-12-22
TIOR APPLICATION NUMBER: 60/253/931
TIOR PILING DATE: 2001-02-16
TIOR SEQ ID NOS: 14110
TION FILING DATE: 2001-02-16
TION RELIGATION NUMBER: 60/250/931
TIOR PILING DATE: 2001-02-16
TION RELIGATION NUMBER: 60/250/931
TIOR PILING DATE: 2001-02-16
TION RELIGATION NUMBER: 60/250/9308
TION RELIGATION
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                                                                                                                                                               Ance 6795, Application US/09815242
nt No. US20020061569A1
RAL INPORMATION:
LICANT: Haselbeck, Robert
LICANT: Zyskind, Judith W.
LICANT: Wall, Daniel
LICANT: Carr, Grant J.
LICANT: Carr, Grant J.
LICANT: Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : DNA
NISM: Enterococcus faecalis
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5-242-6795
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cal Similarity:
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ATION: (1).
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FILING DATE: 04-May-2000 CLASSIFICATION: «Unknown) PRIOR APPLICATION DATA: APPLICATION NUMBER: 60/046,655 FILING DATE: 1997-05-16 APPLICATION NUMBER: 60/044,031 FILING DATE: 1997-05-06 APPLICATION NUMBER: 60/066,009 FILING DATE: 1997-05-06 APPLICATION NUMBER: 40,030 REGISTRATION NUMBER: 40,302 REGISTRATION NUMBER: 40,302 REFERENCE/DOCKET NUMBER: PB369 TELECOMMUNICATION NIPORMATION: TELEPHONE: (301) 309-8504 TELEPHONE: (301) 309-8512 INFORMATION FOR SEQ ID NO: 532: SEQUENCE CHARACTERISTICS: LENGTH: 1283 base pairs TYPE: nucled caid SEQUENCE CHARACTERISTICS: LENGTH: 1283 base pairs TYPE: nucled caid SEQUENCE DESCRIPTION: SEQ ID NO: 532: US-09-070-227A-532	190 Some 190 Some	Db 332GGGGGAAAGGATTAÀNTCAAGCTGTTGGCTTAACCAAACTGGGCCAT 379 Oy 66 AsnalaArgLeuValGlyLeuThrGlylleAspaspalaAlaArgAlaArgAlaEuSer 85
98 AspValAsnValLysCysAspPheValSerValProThrHisProThrIleThrLysLeu 107 138 GAAATTAATTTA	195 AsnLeuSerGluPheGlualaValValGlyLysCysLysThrGluGluGluIleValGlu 2	Oy 294 ValValGlyLysLeuGlyThrSerThrValSerProIIeGluLeuGlu 309 :: :: SEG ACTGTTCAACGTTTGGAGCCCAACCTTCGATTCCTTATCAACACACAA 903 RESULT 8 US-00-070-927A-532 Sequence 532, Application US/09070927A Patent No. US20020120116A1 Patrick J. Dillon Patrick J. Dillon Patrick J. Dillon Steven Barash Patrick J. Dillon Steven Barash TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides NUMBER OF SEQUENCES: 982 CORRESPONDENCES: 982 CORRESPONDENCES: 982 CORRESPONDENCES: 982 CONTRESPONDENCES: 9410 Key West Avenue CITY: ROCKVILLE STATE: Maryland COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COMPUTER READABLE FORM: MEDIDM TYPE: Diskette, 3:50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDCS version 6.2 COMPUTER: ASCII Text CURRENT APPLICATION DATA: APPLICATION DATA:

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GAAACATATTTATTGGGGGAGTGTGGGGAATGGCGCCTGGGGCT&TGATGATTA 6760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5558 AGTGCGATTGATAGTACGATTGCAGCGTTTAAAATTGCTAAAAAAGGAGGCGTCAAAACG 6499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----PheGluGluGlyPheGluGlyValAspProGlnProLeuHis 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluArgileAsnGlnAlaLeuSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLys 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuIleAspPro-----LysGlyThrAspPheGluArgTyrArgGlyAlaThr 190
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                                                                                                                                                                                                                                                                                                                                    29 ThrSerArgIleSerProGluAlaProValProValValLysValAsnThrIleGluGlu 48
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5498 ATTTTAAATCCCGCACCTGCGTTAGAACAAGTTCCTGAAGAATTACTAAAACGTGACAGAT
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158
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Conservative:
Mismatches:
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                                                                                                                                               Length:
                                                                                                                                                                                                                                 Indels:
                                                              ID NO: 4:
  TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ
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182.50
41.09%
22.13%
7.63%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Charles A. Kunsch
APPLICANT: Charles A. Kunsch
Aptican J. Dillon
Steven Barash
TITLE OF INVENTION: Entercoccus faecialis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                    1016 GCAGCCATTCAAATAGCAATTCAGGCTGCAGGATTTTCAGTTTCTAAAGAAGGGGTGATT 1075
                                                                                                                                                                                                                                                                                                                                    955
                                                                                                                                                    ACTGGTACATTAGAAGAAAAGCGGCGTACTTCTTAGAAATGGGCGTAAAAAATGTC--- 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 GluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLysLeuGlyThr--- 300
707 AAACCAGCTGCTATTCATCATATTCCAGTGAATATACTAGAAAAGGTTGATTT----- 760
                                                                                                                                                                                                                                   AlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGlu 281
                                                                                                                                                                                                         AspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeuGln 241
                                                                                                                                                                                                                                                                                         242 ProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGly 261
                                          TyrArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPheGluAlaValGlyLys
                                                                         -----TTCATTCCCAATGAAGATGAATTATTGGAACTTCAACCAGAT
                                                                                                                        CysLysThrGluGluGlu------IleValGluArgGlyMetLysLeulleAla
                                                                                                                                                                                                                                                                                                                                  ACACCCCAAGTGTGCCACTATTTCCCTGCAACAGAAAATATAGCTGTGGATAGCACTGGT
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb sto
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION: CURNOWN>
PRIOR APPLICATION UNMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/046,031
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/046,031
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14
ATTORNEY-AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1076 GATTCTTTAGTTGATCACGTCACTTTGGAAAAT 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---SerThrValSerProIleGluLeuGluAsn 310
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REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09070927A Patent No. US20020120116A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGIH: 6948 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Maryland
COUNTRY: USA
ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-070-927A-4/C
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US-09-912-020-325 (1-477) x U	Db 291 CGTTCTCGCAGACGCGACAACAGCATTATCGTCGTCAAAGGGGCCAAATGACCATGTCAC 350
	116 ulleargLeuaspPheGluGluGlyPheGluGlyValaspProGlnProLe ::::
Score: Percent Similarity: 40.588 Best Local Similarity: 27.278	Db 252 GGAACCGGTTACAGGTCAGGAAAGCGGAACCGCACATAT 290
ent Scores: No.:	96 1SerValProThrHisProThrIleThrLysLeuArgValLeuSerArgAsnGlnGlnLe
; ORGANISM: Bacillus lichen: US-09-974-300-839	Oy 76 paspalahigalaLeuSerLysSerLeualaAspValAsnValLysCysAsppheVa 96
; SEQ ID NO 839 ; LENGTH: 888 ; TYPE: DNA	
SOFTWARE: FASTSEQ for Wind	Qy 56 lalaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAs 76
; PRIOR APPLICATION NUMBER:	72 CGGAGAAACGGTGGCGAATCTTTTAAAACGGTTCCGGGGGGGG
; PRIOR APPLICATION NUMBER: ; PRIOR FILING DATE: 2000-10	Qy 39ProvalValLysValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnVa 56
CURRENT APPLICATION NUMBER CURRENT FILING DATE: 2001	QY ZU MECLERASPARGIYITELYYLOKINESERIG-LLESSERFYGGLUALAFIOVAL 38
; TITLE OF INVENTION: Methods; TITLE OF INVENTION: Expres	-09-912-020-325 (1-477) x US-09-974-300-747 (1-880)
; GENERAL INFORMATION: ; APPLICANT: Berka, Randy M. : APPLICANT: Clausen: Ib Gr.	Indels: Gaps:
US-09-974-300-839 ; Sequence 839, Application US ; Patent No. US20020146721A1	181.50 larity: 40.58% imilarity: 27.27%
Db 828 CGCGCACAAGGCGGCATGC	lignment Scores:
Qy 298 uGlyThrSerThrValSer) TIRE: DNA) ORGANISM: Bacillus licheniformis IIS-09-974-300-747
Db 768 AAGCATCGAATCTGCCTTGC	; SEQ ID NO 747 ; LENGTH: 880
Oy 278 nSerLeuGluGluAlaCysi	; NUMBER OF SEQ ID NOS: 8481 ; SOFTWARE: FastSEQ for Windows Version 4.0
Db 708 TACGACGCCCGGAGAC	; PRIOR APPLICATION NUMBER: 60/279,526 ; PRIOR FILING DATE: 2001-03-27 ; MINDED OF SEC IN NOC. 0401
Oy 258 pValThrGlyAlaGlyAsp	; PRIOR APPLICATION NUMBER: 09/680,598 ; PRIOR FILING DATE: 2000-10-06
DD 651 CTATCACAATGGTCTGC	; CURRENT APPLICATION NUMBER: US/09/974,300 ; CURRENT FILING DATE: 2001-10-05
Qy 238 rLeuLeuGlnProGlyLys	; TITLE OF INVENTION: Expression ; FILE REFERENCE: 10085.500-US
OY 218 SEGUITEATAASPIYIGIUI DD 607TATCCG	; APPLICANT: Berka, Kandy M. ; APPLICANT: Clausen, Ib Groth ; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
555	; Patent No. US20020146721A1 ; GENERAL INFORMATION:
Qy 199 eGluAlaValValGlyI	KESULT 10 US-09-974-300-747
DD 501 TCGCTACGCCGGAAACGC	194 CATTITE
Qy 179 sGlyThrAspPheGluArg1	348 ValPheAspileLeuHisAlaGly
466	Db 6021 ATT
DD 411 GCAGGAGATICCGGAAGAAAAAAAAAAAAAAAAAAAAAAA	Qy 328 LeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysValValMetThrAsnGly 347
150	
Db 351 ACCTGAATACGTTCAAAAAA	OLFI GCGICLICGIIGNCIGIICANCGIIIIGGGGCCCCANCCIICGGIICCIITAICANCANCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Qy 133 uHisGluArgIleAsnGlnP	Db 6141 GCGTCTTCGATGTTTTGGAGCCCAACCTTCGATTCCTTATCAACAGAA 6082

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238
                                                                                   ----SerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGl 162
                                                                                                                            G---GAGAAGCIGTICALCACAGAAGGGAAAAAAGGGGGTCCG 650
                                                                                                                                                                                                                                                                                                   pThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAs 278
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GlnAlaLeuSerSerIle-----GlyAlaLeuValLeu---- 149
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 MetLeuAspArgTyrTrpTyrGlyProThrSerArg-IleSerProGluAlaProVal-- 38
                76 pAspAlaAlaArgAlaLeuSerLysSerLeuAlaAspValAsnValLysCysAspPheVa
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                                                        39 ----ProvalvalLysValAsnThrIleGluGluArgProGlyGly---AlaAlaAsnVa
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Patent No. US20020061569A1
GENERAL INFORMATION:
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Zyskind, Judith W.
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W
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APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yammonco, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: PEOKARYOES
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 00/09/815,242
CURRENT FILING DATE: 2001.03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000.03-21
PRIOR FILING DATE: 2000.05-23
PRIOR FILING DATE: 2000.05-23
PRIOR FILING DATE: 2000.05-26
PRIOR FILING DATE: 2000.10-23
PRIOR FILING DATE: 2000.10-23
PRIOR FILING DATE: 2000.11-27
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR FILING DATE: 2000.11-27
PRIOR FILING DATE: 2000.11-27
PRIOR APPLICATION NUMBER: 60/25/,931
PRIOR FILING DATE: 2000.12-22
PRIOR FILING DATE: 2000.12-22
PRIOR FILING DATE: 2000.03-1410
SOSTWARE: FESTEED FOR WINDOWS VERSION 4.0
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LENGTH: 921
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670 TTAGGAAGTCGTGGTGTATGGCTAGCGTGAATGGTGAAGGTCAG----CGCGTTCCTGGA
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TITLE OF INVENTION: Identification of Essential Genes in
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APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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Zyskind, Judith W.
Wall, Daniel
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) NAME/KEY: CDS
; LOCATION: (1)...(933)
US-09-815-242-9878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 9878
LENGTH: 933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAspPheGluGluGlyPheGlu 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyValAspProGlnProLeuHisGluArgIleAsnGlnAlaLeuSer----- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 GGTGAGAATGTCATCGGTATTCATGCCGGCGCTAATGCTGCCCTTTCCCCGGCGCTGGTG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyAlaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArgLysAlaGlyValProVal 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaAspValAsnValLysCysAspPheValSerValProThrHisProThrIleThrLys 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GATATTACTCCG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376 GAAGCGCAACGTGAGCGTATTGCCAACGCGTCAGCATTATTAATGCAG-----CTGGAA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 ---CTTAATCTTCAATCTTTCCTACTCCAGGGGAAACCGTAACCGGTAACCACTATCAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 ATCGCGTTTAFTGCCTGTACGGGTGATGACAGCATTGGTGAGAGCGTTCGCCAGCAGCTC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------SerIleGlyAlaLeuValLeuSerAspTyrAlaLys 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 ProThrSerArgIleSerProGluAlaProValProValValLysValAsnThrIleGlu 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 GluArgProGlyGly---AlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsn 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 AlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeu 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 GluArgAlaGlyValMetValVal --- GlyAspValMetLeuAspArgTyrTrpTyrGly 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ::: ||||||| :::|||||| ||| ||| ||| 4 CAAAACGCAGGGGGCACTTGGCAGGATTAATGCTGACCACATT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/200,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-27
PRIOR PLING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR APPLICATION NUMBER: 60/25,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2000-12-2
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASSESE FOR WINDOWS VERSION 4.0
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169.00
39.49%
24.52%
7.06%
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; LOCATION: (1)...(930)
US-09-815-242-6309
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 930
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510 GATGCAGCGAAGGCGGCGCGCGGCACTGCATGAAAAGGTATCCGTACTGTACTGATACT 669
                                                                                                                                                                                                                                                               727 TTCCGGGTGCAGGTGTCGATACCATTGCTGCCGGAGATACCTTTAACGGTGCGTTAATC 786
430 TCACCACTCGAAAGTGTGATGGCAGCGGCGAAAATCGCCCCATCAAAAFAAGACTATCGTT 489
                                                                    -----LysGlyThrAspPheGluArgTyrArgGlyAlaThrLeu 191
                                                                                                                                                                                                                                                                                                                                                           212 IleValGluArgGlyMetLysLeuIleAlaAspTyrGluLeuSerAlaLeuLeuValThr 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 ArgSerGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThr 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 GlnAlaGlnGluValTyrAspValThrGlyAlaGlyAspThrVallieGlyValLeuAla 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             670 TTAGGAAGTCGTGGTGTATGGGCTAGCGTGAATGGTGAAGGTCAG---CGCGTTCCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 AlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuThrProAsnLeuSerGluPheGluAlaValValGlyLysCysLysThrGluGluGlu
                                                                                                                                     GCGCTTAACCCGGCTCCGGCTCGCGAACTTCCTGACGAACTGCTGGCGCTGGTGGACATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 GlyValValValGlyLysLeuGlyThrSerThrValSerPro 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        847 GCGATTGCCGTAACACGTAAAGGCGCCACAACCTTCCGTACCG 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Obligation, August Applicant: Applicant: Applicant: Obligation, Judith W. Applicant: Zyskind, Judith W. Applicant: Trawick, John D. Applicant: Trawick, John D. Applicant: Trawick, John D. Applicant: Yamanoco, Robert T. Applicant: Xu, H. Howard TITLE OF INVENTION: Identification of Essential Generative OF INVENTION: Prokaryotes
TITLE OF INVENTION: DACARYOTES
TITLE OF INVENTION: DACARYOTES
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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Patent No. US20020061563A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14110
                                                                175 LeuIleAspPro-
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Search completed: November 27, 2002, 02:57:12 Job time : 130 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 26, 2002, 20:59:44 ; Search time 3602 Seconds
(without alignments)
3329.530 Million cell updates/sec
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Title:

US-09-912-020-325
Perfect score: 2393
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Ygapop 6.0 , Ygapext 7.0
Delop 6.0 , Delext 7.0
Searched: 24791104 seqs, 12571243825 residues
Total number of hits satisfying chosen parameters: 49582208

Minimum DB seq length: 0

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-TRANS-human40.cdi -LIST-45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-MAXLEN-200000000 -USER-US09912020_@CGN_1_1_3142_@runat_25112002_091429_24305
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELON=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

MARIES	
SUM	

Description	Sequence 6204, Ap Sequence 165, App Sequence 276, App Sequence 6204, Ap Sequence 165, App Sequence 6204, Ap
ID	PCT USO2-03987-6204 US-09-492-709A-165 US-09-741-669-276 US-09-815-242-6204 US-09-912-020-165 US-10-072-851-6204
DB	118 129 34 39
å Query Match Length DB	1434 1434 1434 1434 1434 1434
% Query Match	100.0 100.0 100.0 100.0
Score	2393 2393 2393 2393 2393
Result No.	H 2 W 4 W 0

US-09-912-020-325 (1-477) x PCT-US02-03987-6204 (1-1434)	alThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMe	Db 1 ATGAAAGTAACGCTGCCAGAGTTTGAACGTGCAGGAGTGATGGTGGTGGTGGTGGTGTGGTGTGTGT	euAspArgTyrTrpTyrGlyProThrSerArg1leSerProGluAlaProValProVa	Db 61 CTGGATCGTTACTGGTACGCCCCACCAGTATCTCGCCGGAAGCGCCGGTGCCCTG 120	alLysValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIl	GGCGATGAAT	Oy 61 AlaSerLeuGlyAlaAsnAlaArgLeuValGlÿLeuThrGlyIleAspAspAlaAlaArg 80	rcegrectantecacecregresegridacesecarreaceses	Oy 81 AlaLeuSerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThr 100	GTAAATCTCTGGCCGACGTCAACGTCAAATGCGACTTCGTTTCTGT	Qy 101 HisProThrIleThrLysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAsp 120	CCATTACCAAATTACGGGTACTTTCCCGCAACCAACAGCTGATCCGTCTGG	heGluGluGlyPheGluGlyValAspProGlnProLeuHisGluArgIleAsnGlnAl		euSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGly	TIGHTH THE THE THE THE THE THE THE THE THE	Qy 161 GlnGlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeulleAspProLysGly 180	Arccaacreeceraaaeceererreearecrearear	Oy 181 ThraspPheGluargTyrargGlyalaThrLeuLeuThrProAsnLeuSerGluPheGlu 200	laValValGlyLysCysLysThrGluGluGluIleValGluArgGlyMe	Db 601 GCTGTTGTCGGTAAATGTAAGACCGAAGAAGAGATTGTTGAGCGCGCGC	Oy 221 AlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeu 240	2C v4m[cVxxxxvvvvvvvvvvvvvvvvvvvvvvvvvvvvvvvvv			Oy 261 GIYALGGIYASPINIYATILEGGIYVALLEUALAALATIITILEGALAAGISGIYASBSELDU 280	/ 01	CY 281 GLUGLUALACYSPREPREALARANAALAGATYVALVALVALGAYSEUGLYTH 300 DD 841 GAAGAAGCCTGCTTCTTTGCCAATGGGCGGGTGGCGTGGGGGGGG	301. SerThrValSerProIleGluteuGluAsnAlaValArdGlvArdAlaAspThrGlvPhe 32	901 TCCACGGTTCGCCGATCGAGCTGGAAATGCTGTACGTGGACGTGCAGATACAGCTTT 9	321 GlyValMetThrGluGluGluLeuLySLeuAlaValAlaAlaAlaArgLySArgGlyGlu 340	961 GGCGTGATGACCGAAGAGGAACTGAAGCTGGCCGTAGCGGCAGCGCGTAAACGTGGTGAA 10	Oy 341 LysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeu 360
9 16 US-09-252-691-3421 Sequence	2265 94.7 1434 1 PCT-US02-03987-9661 Sequence 9661, 2265 94.7 1434 31 US-09-815-242-9661 Sequence 9661, 2365 94.7 1434 31 US-09-8164 9661 Sequence 9661, 2365 94.7 1434 31 US-09-8164 9661 Sequence 9661, 2365 94.7 1434 31 US-09-8164 9661 9661, 2365 9661,	2227 93.1 1500 18 US-09-489-039A-2037 Sequence 2037,	14 1968 82.2 27693 33 US-09-897-516-1461 Sequence 1461,	1968 82.2 2/693 33 US-09-89/-516-1462 Sequence 1462, 1968 82.2 2/693 33 US-09-89/-516-1463 Sequence 1463, 1968 82.2 2/693 31 US-09-897-516-1463 Sequence 1463,	18 1968 82.2 27693 33 US-09-897-516-1465 Sequence 1465,	1908 82.2 2/093 33 US-09-897/-510-1460 Sequence 1400, 20 1968 82.2 2/7693 33 US-09-897/-516-1467 Sequence 1467, 31 1068 97 2 27603 33 US-09-807-516-1467 Sequence 1467, 31 1068 97 2 27603 33 US-00-807-516-1467 Sequence 1460	22 1968 82.2 27693 33 US-09-897-516-1469 Sequence 1470, 23 1968 82.2 27693 33 US-09-897-516-1469 Sequence 1470,	24 1968 82.2 27693 33 US-09-897-516-1471 Sequence 1471, 25 1968 82.2 27693 33 US-09-897-516-1472 Sequence 1472.	1968 82.2 27693 33 US-09-897-516-1473 Sequence 1473,	1968 82.2 27693 33 US-09-897-516-3226 Sequence 3226, 1968 R2 2 27693 33 US-09-897-516-3226 Sequence 3227,	1968 82.2 27693 33 US-09-897-516-3228 Sequence 3228, 1968 82.2 27693 33 US-09-897-516-3228 Sequence 3228, 2228	1968 82. 2.7693 33 US-09-897-516-3230 Sequence 3230, 1968 82. 2.7669 33 US-09-897-516-3230 Sequence 3230, 1968 82. 2.7663 33 US-09-807-516-3231	1968 82.2 2/093 33 US-09-097-516-3332 Sequence 5234, 1968 03 3 726-09-09-09-09-09-09-09-09-09-09-09-09-09-	1968 82.2 27693 33 US-09-09/-516-3233 Sequence 3233, 1968 03.2 276693 33 US-09-89/-516-3234 Sequence 3234, 1969 03 3 37663 23 US-06-067-516-2335	34 1968 82.2 27693 33 05-09-897-516-5253 Sequence 5259,	39 1908 82.2 2/093 03 US-00-213-101-1461 Sequence 1461, 40 1968 82.2 2/563 65 US-60-215-161-1462 Sequence 1462, 41 1060 03 3 27603 65 US-60-216-1462	1900 02.12 2/053 05 05 00 215 101 1405 Sequence 1405, 1968 82.2 27693 65 US-60-215-161-1464 Sequence 1464, 1968 82.2 27693 65 US-60-215-161-1465 Sequence 1465,	44 1968 82.2 27693 65 US-60-215-161-1466 Sequence 1466, 45 1968 82.2 27693 65 US-60-215-161-1467 Sequence 1467,	ALIGNMENTS	RESULT 1	PCT-US02-03987-6204; ; Sequence 6204, Application PC/TUS0203987 : GRNTPA1 INFORMATION:	<pre>// APPLICANT: Elitra Pharmaceuticals, Inc. // TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits C // TITLE OF INVENTION: Proliferation</pre>	FILE REFERENCE: ELITI			; NUMBER OF SEQ ID NOS: 15811 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEO ID NO 6204	LENGTH: 1434	irre: DNA ; ORGANISM: Escherichia coli : FFATURE:	; NAME/KEY: CDS : LOCATION: (1) (1434)	PCT-US02-03987-6204	1.09e-204 2393.00	ilarity: 100.00% conservative: Similarity: 100.00% Mismatches:	100.00% Indels: 1 Gaps:

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US-09-492-709A-165
Sequence 165, Application US/09492709A
GENERAL INFORMATION:
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Forsyth, R. Allyn
APPLICANT: Froelich, Jamie M.
APPLICANT: Froelich, Jamie M.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Wansard
TITLE OF INVENTION: ESCHERICHIA COLI
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA, O01A
CURRENT APPLICANT: BLITRA, O01A
CURRENT APPLICANT: NUMBER: US/09/492,709A
CURRENT APPLICANT: NUMBER: US/09/492,709A
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-492-709A-165
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Matches:
Conservative:
Mismatches:
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E. coli
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Control of E. Col
FILE OF INVENTION: Genes identified as req
TITLE OF INVENTION: Proliferation of E. Col
FILE REFERENCE: ELITRA.009A
CURRENT APPLICATION NUMBER: US 60/173005
PRIOR APPLICATION NUMBER: US 60/17305
PRIOR FILING DATE: 1999-12-23
PNUMBER OF SEQ ID NOS: 481
SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local Similarity:
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US-09-741-669-276
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LENGTH: 1434
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 LeuSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerVal
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US-09-815-242-6204
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AAACGGCTGAAAGGGGATTCCCGCCCGGTAAACCCACTCGAACAGCGTATGATTGTGCTG 1200
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   AlaValValGlyLysCysLysThrGluGluGluIleValGluArgClyMetLysLeuIle
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Mismatches:
Indels:
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Matches:
                                         APPLICANT: TRANICA, JOHN D.
APPLICANT: TRANICA, ROBERT T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: DECRATYORS
FILE REFERENCE: ELITRA 011A
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/205,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 6204
LENGTHER. PASSEG FOR WINDOWS VERSION 4.0
SEQ ID NO 6204
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100.00%
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Escherichia coli
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Best Local Similarity:
Query Match:
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US-09-815-242-6204
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Sequence 165, Application US/09912020
GENERAL INFORMATION:
APPLICANT: Dyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsith, R. Allyn
APPLICANT: Carr, Grant J.
APPLICANT: Tammoto, Robert T.
APPLICANT: Yamamoto, Robert T.
FILIR REFERENCE: ELITRA.001DV1
CURRENT APPLICATION NUMBER: US/09/912,020
CURRENT FILING DATE: 2000-01-27
RRIGN FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FastSEQ for Windows Version 3.0
MANDEL DATE: 1434
MANDEL DATE: 1434
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Matches:
Conservative:
Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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ORGANISM: E. Coli
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Sequence 6204, Application US/10072851
Sequence 6204, Application US/10072851
SEQUENCE INFORMATION:
APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Foundies, J. Gordon
APPLICANT: Application
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: YSskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
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GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO F
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
SEQ ID NO 3421
LENGTH: 1449
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   AlaValValGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle
              GCTGTTGTCGGTAAATGTAAAGACCGAAGAAGAGATTGTTGAGCGCGCGTGAAACTGATT
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) ORGANISM: Enterobacter cloacae
US-09-252-691-3421
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APPLICANT: Yamamoto, Robert T.

APPLICANT: Roemer, Terry
APPLICANT: Roemer, Terry
APPLICANT: Janag, Bo
APPLICANT: Boone, Charles
APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying the Target of a Compound which Inhibits of INVENTION: Methods for Identifying the Target of a Compound which Inhibits of INVENTION: Methods for Identifying the Target of a Compound which Inhibits of INVENTION: MUMBER: US/10/072,851
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6204
LENTH: 1434
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Matches:
Conservative:
Mismatches:
Indels:
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; NAME/KEY: CDS
; LOCATION: (1)...(1434)
US-10-072-851-6204
                                                                                                                                                 TYPE: DNA ORGANISM: Escherichia
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Query Match:
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s: 452 vative: 19 ches: 5 : 0	(1-1449)	EValv 3GTTG	eSerProGluAlaPro 	gProGlyGlyAlaAlaAsnVal 	yLeuThrGlyIleAspAspAlaA 	LysCysAspPheValSer' 	erargasnGlnGlnLeulleAr 	nProLeuHisGluArgIleAsm :	AlaLysGlyAlaLeuAl 	Provalleuil 	ThrProAsnLe	eValGluArgGly : GGTTGAGCGCGGC	SerGluGlnGlyMetS 	GlnalaGlnGluValTy 	aThrLeuAlaAlaC 	valvalGl	ArgGlyArg GrGGGCG
Matches Conserv Mismatc Indels: Gaps:	252-691-3421	GluargalaGly 	/ProThrSerargile 	ArgProGlyGly 	ArgleuValGlyLeu 	AsnVa AATGT	gValLeuSerArg 	/ValAspProGlnPro 	alLeuSerAspTyral	ArgLysalaGlyval	GlyAlaThrLeuLeu 	luGluGluIl 	LeuValThrArgs 	ProThr CCAACC	LLeuAlaAl 	eAlaAsnAlaAlaAlaGlyVal 	GluLeuGluAsnAlaVal
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milarity: Similarity: h:	020-325 (1-47	MetlysValThrLeuProGluPheGluArgAlaGlyValMe 	LeuAspArgTyrTrp 	ValLysValAsn: GTAAAGGTCGAC	AlaSerLeuGlyAlaAs 	AlaLeuSerLysSe 	HisProThrile' 	PheGluGluGly TTTGAAGAAGGG	LeuSerSerile(TGGGCAATATT	GlnGlnMetIle(ThraspPheGluard	AlavalvalGly) cccrcccccc	AlaAspTyrGluLeu ::: GCTGATTTCGAGCTC	GlnProGlyLysi 	GlyAlaGlyAsp' 	GluGluAlaCysP 	SerThrValSer TCCACCGTTTCG
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RESULT 8

US-09-252-691C-3421

Sequence 3421, Application US/09252691C

SEQUENCE 3.1. Application US/09252691C

GENERAL INFORMATION:

APPLICANT: Keith G. Weinstock et al.

TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO ENTEROBACTE

TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.135

CURRENT APPLICATION NUMBER: US/09/252,691C

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-24

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 11326

SEQ ID NO 3421

SEQ ID NO 3421
                                          1099 GCGAATGCGCGCAAGCTGGGCGACCGCCTGATTGTGGCGGGTCAACAGCGATGCCTCAACC 1158
                                                                                       361 AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr 380
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Matches:
                                                     APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard.
TITLE OF INVENTION: Identification of Essent:
TITLE OF INVENTION: Identification of Essent:
TITLE OF INVENTION: PROKATYOLES
TITLE OF INVENTION: PROKATYOLES
FILE REFERENCE: ELITRA OLIA
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PRILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
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  Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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US-09-815-242-9661
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Sequence 9661, Application US/09815242

οy	121 E	PheGluGluGlyCheGluGlyValAspProGlnProLeuHisGluArgIleAsnGlnAla 140	US-10-072-851-9
Q	361 1	ITTGAAGAAGGCTTTGAGGGCGTGGACCCGCAGCCGTTGCATGAGCGTATCAACCAGGCG 420	GENERAL INFO
οy	141 1	LeuSerSerIleGlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerVal 160	APPLICANT:
QQ	421	TGGGATCGATCGCGCGCTGTTTTTTTTTTTTTTTTTTTT	, APPLICANT:
οy	161	GinGinMetileGinLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGly 180	APPLICANT: APPLICANT: APPLICANT:
qq	481	CAGACTATGATTTCCCTAGCGCGCCCCAGGGGGGCGTGCCGCTCTCATCGATCG	APPLICANT
οy	181	ThraspPheGluargTyrargGlyalaThrLeuLeuThrProAsnLeuSerGluPheGlu 200	APPLICANT
qq	541 7	ACGGATTTTGAACGTTACCGCGCGCCCACGCTGCTGACCCTTTCTGAATTCGAG 600	APPLICANT: APPLICANT:
Oy	201 4	AlaValValGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIle 220	APPLICANT: ; APPLICANT: . TITLE OF IN
qq	601	SCGGTTCCGGGGAAATGTAAAAGCGAACGGACTGGTTGAACGCGGCATGAAGCTCATT 660	TITLE OF IN
Qy	221 #	AlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeuLeu 240	CURRENT APP
q	661	SCCGATTACGACCTTTCCGCGCTGTTGGTCACGCTGTTCCGAACAGGGAATGACGCTGCTG 720	PRIOR APPLIC
٥y	241 (GInProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThr 260	, NUMBER OF SI
QQ	721	CAACCGAATAAAGCGCCGCTACATATGCCGACGCGCGGGGGGTTTATGATGTTACC 780	S
ογ	261 0	GlyAlaGlyAspThrVallleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu 280	TYPE: DNA
q	781	SGTGCGGGCGATACGGTGATCGGCGTGCTGCGGCGGCGGCGGGGGGGG	FEATURE:
δ	281	GluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLysLeuGlyThr 300	- 1
qq	841	3AGGAGGCGTGTTATTTCGCCAATGCGGCGGCGGCGTAGGTAG	10-7/0-01-80
Οy	301 8	SerThrValSerProIleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPhe 320	Alignment Score Pred. No.: Score:
g G	901	TCAACGGTTTCCCCTATTGAGCTGGAAAACGCAGTGCGCGGACGCGGGATACCGGCTTC 960	Percent Similar
οy		GlyvalMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGlu 340	Query Match: DB:
g	961 (GGCGTCATGACCGAAGAGGAGTTGAGACAGGCCGTCGCCAGCGCGCGTAAGCGTGGCGAG 1020	020-615-05-BI
ογ	341 1	LysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeu 360	
q	1021	naagtggtcatgaccaacggcgtttcgatattctgcacgcgggccacgtctcttatctg 1080	
δ		AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr 380	21
g	1081	SCGAACGCGCGCAAACTGGGCGACCGCCTGATTGTTGCGGTCAATAGTGACGCCTCGACT 1140	- 5
δλ		LysArgLeuLysGlyAspSerArgProValAsnProLeuGluGluGlnArgMetIleValLeu 400 	41
QO .			 DD 121 GTTA
à á	401	GlyAlaLeuGluAlaValAspTrpValValSerPheGluGluAspThrProGlnArgLeu 420	Oy 61 Alase
3 8		7	Db 181 GCGTC
S 8	421	IIEAAGLIVIIELEUKTOASPLEULGUVALLYSGIJGIJABSTYTLYSKTOGLUGIDIIE 440 	Oy 81 AlaLe
ô		4	Db 241 GCGC
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δ	461	3lyCysSerThrThrAsnIleIleLysLysIleGlnGlnAspLysLys	Db 301 CATC
ф	1381		-
RESU	RESULT 11		Db 361 TTTG

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Bussey, Howard States and States of a Compound which Inhibit WENTION: Methods for Identifying the Target of a Compound which Inhibit ENVENTION: Proliferation ENVENTE: ELITRA.028A
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/10/072,851
PLICATION NUMBER: 60/267,636
LING DATE: 2001-02-09
F SEQ ID NOS: 15811
F FastSEQ for Windows Version 4.0
1434
51, Application US/10072851
DRMATION:
                      Carr, Grant J.

Xu, H. Howard

Foulkes, J. Gordon
Zamudio, Carlos
Haselbeck, Robert
Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Yamamoto, Robert T.
Roemer, Terry
Jiang, Bo
Boone, Charles
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TITLE OF INVENTION: NUCLEIC ACLD AND CHOLNEY.
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTIVE FILE REFERENCE: 2709.2004.001
CURRENT APPLICATION NUMBER: US,09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 2037
                                                                              pneumoniae
                                                                                                         9.54e-190
2227.00
97.47%
92.19%
93.06%
                                                                       TYPE: DNA
ORGANISM: Klebsiella
                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                     US-09-489-039A-2037
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DB:
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; Sequence 2037, Application US/09489039A
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NN: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
NN: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
2709.2004001
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US-09-912-020-325 (1-477) x US-09-543-681A-2462 (1-147)	Qy 1 WetLysValThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMet 20	Qy 21 LeuaspargTyrTrpTyrGlyProThrSerarg1leSerProGlualaProValProVal 40	Oy 41 ValLysValAsnThrIleGluGluArgProGlyGlyAlaalaAsnValAlaMetAsnIle 60 	Oy 61 AlaSerLeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArg 80 	Qy 81 AlaLeuSerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThr 100	Qy 101 HisProThrIJeThrLysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAsp 120	Oy 121 PheGluGlyPheGluGlyValaspProGlnProLeuHisGluargIleAsnGlnAla 140	Oy 141 LeuserSerIleGlyAlaLeuValLeuserAspTyrAlaLysGlyAlaLeuAlaserVal 160	Qy 161 GinglinMetileGinLeualaArgLysAlaGlyValProValLeuileAspProLysGly 180	Oy 181 ThraspPheGluargTyrargGlyalaThrLeuLeuThrProAsnLeuSerGluPheGlu 200 :::	Qy 201 AlavalValG1yLysCysLysThrGluGluGluLleValGluArgG1yMetLysLeulle 220	Oy 221 AlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGluGluGletSerLeuLeu 240 11	Qy 241 GlnProGlyLysalaProLeuHisMetBroThrGlnAlaGlnGluValTyrAspValThr 260	Oy 261 GlyAlaGlyAspThrVallleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu 280	Oy 281 GluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValValysLeuGlyThr 300	Oy 301 SerThrValSerProIleGluLeuGluAsnalaValArgGlyArgAlaAspThrGlyPhe 320	Qy 321 GlyvalMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGlu 340	Qy 341 LysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeu 360 :::::
Db 787 CAGCCGGGACGTCCGCCGCTGCATATGCCGAGGCCCAGGAAGTGTACGAGGCGTGACC 846	Oy 261 GlyAlaGlyAspThrVallleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeu 280	Oy 281 GluGluAlaCysPhePheAlaAshAlaAlaGlyValValValGlyLysLeuGlyThr 300	Qy 301 SerThrValSerProIleGluLeuGluAsnalaValArgGlyArgAlaAspThrGlyPhe 320	Oy 321 GlyvalMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGlu 340 	Qy 341 LysvalvalmerThrasnGlyvalPheAspIleLeuHisAlaGlyHisValSerTyrLeu 360 	Oy 361 AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr 380	Oy 381 LysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMet11eValLeu 400	Oy 401 GlyalaLeuGlualaValAspTrpValValSerPheGluGluAspTrProGlnArgLeu 420 	Oy 421 IlealadlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysProGluGluIle 440	Oy 441 AlaGlySerLySGluValTrpAlaAsnGlyGlyGluValLeuValLeuValDeuAsnPheGluAsp 460 	Oy 461 GlyCysSerThrThrAsn1le11eLysLys1leGlnGlnAsp 474	RESULT 13 US-09-543-681A-2462 ; Sequence 2462, Application US/09543681A	APPLICANT: GARY BRETON TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FITE PERPENDENCE: 3700, 1003,000,000,000,000,000,000,000,000,000	CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT FILING DATE: 2000-04-05 PRICA PIDION NUMBER: US 60/128,706 PRICA FILING DATE: 1000-04-05	NUMBER OF SEQ ID NOS: 8344) ORGANISM: Proteus mirabilis US-09-543-681A-2462	5.51e-170 2007.00 91.33%	Mismatches: Indels: Gaps:

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                                                                                                     GlyAlaLeuGluAlaValAspTrpValValSerPheGluGluAspThrProGlnArgLeu
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                     AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr
                                                             LysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeu
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Matches:
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APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Huesing, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina C.
APPLICANT: Slater, Thomas M.
APPLICANT: Spiridonov, Sergei
TITLE OF INVENTION: Xenorhabdus sp. Genome SG
FILE REPERENCE: 38-21(51847)B
CURRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-06-29
PRIOR FILING DATE: 2000-06-30
NUMBER: OF SEQ ID NOS: 8409
SEQ ID NO 1461
LENGTH: 27693
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Sequence 1461, Application US/09897516
GENERAL INFORMATION:
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; LOCATION: (877)...(1428)
US-09-897-516-1461
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                          IleAlaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysProGluGluIle
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                   APPLICANT COCDIN, David R.
APPLICANT Goldman, Barry S.
APPLICANT Hinkle, Gregory J.
APPLICANT Hinkle, Gregory J.
APPLICANT Huesing, Joseph E.
APPLICANT Krasomil-Osterfeld, Karina C.
APPLICANT Malvar, Thomas M.
APPLICANT Slater, Steven C.
APPLICANTON WHERE: US 60/215, 161
PRIOR RILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 8409
SEQ ID NO 1462
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                       ; Sequence 1462, Application US/09897516 ; GENERAL INFORMATION:
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81.14%
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ORGANISM: Xenorhabdus sp.
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; LOCATION: (1739)..(1870)
US-09-897-516-1462
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Best Local Similarity:
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                                          ThraspPheGluargTyrArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPheGlu
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Search completed: November 27, 2002, 01:55:53. Job time : 3642 secs

Sequence 1809, Ap Sequence 100, App Sequence 45784, A Sequence 45791, A Sequence 27, App1 Sequence 45795, A Sequence 45795, A Sequence 45792, A Sequence 45793, A Sequence 45793, A Sequence 45793, A Sequence 45793, A Sequence 1063, App1 Sequence 32, App1 Sequence 33, App1 Sequence 48, App1 Sequence 10, App1 Sequence 48, App1 Sequence 48, App1 Sequence 48, App1

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APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: BYTERECOCCUGS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT ENERGY 032796-032 CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR PILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 NUMBER OF SEQ ID NOS: 6812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  655 ATGATTGTAGTGGGTAGTTTAAACGTTGATAATTATCTGTATTCAACAAATTTACCACAT 714
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PCT-USO2-32727-16
US-09-134-000C-1809
US-10-264-213-100
US-09-724-676-45781
US-09-724-676-45791
PCT-USO2-32727-21
US-09-724-676-45794
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US-10-02-4114-1063
US-10-271-889-48
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US-09-134-000C-2975
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Sequence 1119, Application US/09134000C
GENERAL INFORMATION:
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US-09-134-000C-1119
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1: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

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5: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO0_NEW_COMB.seq:*
                             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd

    nucleic search, using frame_plus_p2n model

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US-10-092-411A-1684
US-10-092-411A-2723
PCT-US02-32727-56
PCT-US02-32727-107
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US-10-092-411A-2746
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                                                                                                                   66 AsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSer
                                                                                                                                                      CAGGCCACCTTAATTGGTTGTTTAGGCTCAGACACAGATGCGAATTACTTATATAAAGAA
                                                                                                                                                                                      LeuAlaAspValAsnValLysCysAspPheValSerValProThrHisProThrIleThr
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                                                                                                                                                                                                                                                        LysLeuArgValLeuSerArgAsnGlnClnLeuIleArgLeuAsp--------
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                                                                                                                                                                                                                                                                                        901 CGTATTCAAGATACTGAGACTGGTCAAGCTTATATTTTATGTTGAGACAAGCGGCGACTCC
                                                 IleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAla
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APPLICANT: Havukkala, Ilkka J
APPLICANT: Lubbers, Mark William
APPLICANT: Dekker, James
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them, and methods for using them.
1501 GATTCTTTAGTTGATCACGTCACTTTGGAAAAT 1533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5163 ATTGATACCCAATATGTTGCGACCACGCCAGACACGGAAACCGGCCAGGCGTATATTCTG 5104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 AlaAspValAsnValLysCysAspPheValSerValProThrHisProThrIleThrLys 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 GlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeu------AlaSerVal 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 GlnGlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspProLysGly 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ThrAspPheGlu------ArgTyrArgGlyAlaThrLeuLeuThrProAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 SerProGluAlaProValProValValLysValAsnThrIleGluGluArgProGlyGly
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74
57
144
37
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Mismatches:
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                                                                                                                                                                                                                                           Length:
Matches:
                                                                                                                                                                                                                                                                                                                     Indels:
FILE REFERENCE: 11000.1043c3
CURRENT APPLICATION NUMBER: US/10/264,213
CURRENT FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                          TYPE: DNA
CRGANISM: Lactobacilllus rhamnosus
US-10-264-213-15
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170.50
41.99%
23.72%
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Best Local Similarity:
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                                                                                                   SEQ ID NO 15
LENGTH: 7210
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Oy 257 TyraspvalThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAla 275 	Qy 133LeuHisGluArgIleAsnGlnAlaLeuSerSerIleGly 145
Oy 276AlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaGlyValVal 294	Oy 146 AlaLeuValLeuSerAspTyrAlaLysGlyAlaLeu
Qy 295 ValGlyLysLeuGlyThrSerThrValSerProlle 306	Qy 162 GlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeuIleAspPro 178 :::::: ::: bb 475 CAAGCATTAAAATTGCTGTAAAAAATATCACTACTGTATTAAATCCTGCACCGGCA 534
RESULT 3 US-10-092-411A-1684 ; Sequence 1684, Application US/10092411A	Qy 179
APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: BEDDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: PEDEDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: PEDEDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS	Oy 191 LeuLeuThrProAsnLeuSerGluPheGluAlaValGlyLySCySLysThrGluGlu 210 :::::
CURRENT APPLICATION NUMBER: US/10/092,411A CURRENT FILING DATE: 2002-03-07 FIRDA APPLICATION NUMBER: US 09/134,001 PRIOR APPLICATION NUMBER: US 09/134,001	Oy 211 GluileValGluargGlyMetLysLeuIleAlaAspTyrGluieuSerAlaLeuLeuVal 230
FILEN APPLICATION UNBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR FILING DATE: 1897-17-08 PRIOR FILING NUMBER: US 60/055,779	Qy 231 ThrargSerGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisMetPro 250
; FILOR LILING DAIL: 1397 708 14 ; NUMBER OF SEQ ID NOS: 5676 ; SEQ ID NO 1684 ; LENCTH: 948	Oy 251 ThrGlnAlaGlnGluValTyrAspValThrGlyAlaGlyAspThrValIleGlyValLeu 270 ::
11FE: UNA ; ORGANISM: Staphylococcus epidermidis US-10-092-411A-1684	Qy 271 AlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAla 289
Alignment Scores: 1.53e-06 Length; 948 Pred. No.: 165.50 Matches: 77 Percent Similarity: 39.12% Conservative: 56 Rest Local Scinilarity: 20.12% Mismatches: 117	Qy 290 AlaAlaGlyvalValValGlyLysLeuGlyThrSerThrValSerFrolleGluLeuGlu 309
6.92% Indels:	RESULT 4 US-10-092-411A-2723 ; Sequence 2723. Application US/10092411A
	; GENERAL INFORMATION: ; APPLICANT: Lynn Doucette-Stamm et al ; TITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS ; FILE REFERENCE: 032796-101
Oy 22 AspargTyrTrpTyrGlyProThrSerArg1leSerProGlualaProValProValVal 41	; CURRENT APPLICATION NUMBER: US/10/092,411A ; CURRENT FILING DATE: 2002-03-07 ; PRIOR APPLICATION NUMBER: US 09/134,001 ; PRIOR FILING DATE: 1998-08-13
Oy 42 LysValasnThrIleGluGluargProGlyGlyAlaalaasnValalaMetasn 59 :::	; PRIOR APPLICATION NUMBER: US 60/064,964 ; PRIOR FILING DATE: 1997-11-08 ; PRIOR APPLICATION NUMBER: US 60/055,779 ; PRIOR FILING DATE: 1997-08-14
Oy 60 IlealaSerLeuGlyAlaAsnalaArgLeuValGlyLeuThrGlyIleAspAspAlaAla 79 11:	; NOWBER OF SEQ ID NOS: 56/6 ; SEQ ID NO 2723 ; TENGTH: 414 ; TYPE: DMA
Oy 80 ArgalaLeuSerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValPro 99 :::::::::::::::::::::::::::::::::::	411A-2723 Scores:
Oy 100 ThrhisprothrileThrLysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeu 119 Db 268 ATTCAT	1.23e-05 150.00 1arity: 54.68% imilarity: 33.81%
Qy 120 AspPheGluGluGlyPheGluGlyValAspProGlnPro 132 ::: Db 295 GAAAGTGAAGAAACTGGGCAAGCATTTATCACTGTTGATGAAGCAGGACAAAATACGATT 354	Indels: Gaps:)-092-411A-2723 (1-414

Db 2512 AGGTCGGCGTGGAGAGTTTCCGGCCCCAGGGGAGACCTTGGCCGCGGGGGACA 2571 Qy 48 GluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsn 66	Oy 107 LeuArgValLeu	2962 197 3004 211 3061 231 3121 251 3181 271	291 AlaGlyvalValValValOlLysLeuGlyThrSerThrValSerProlleGluLeu
ValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValS AGTCATTACTTAGGTACATATGACTTGCTTCATTATGGTCATATIS:: AGTCATTACTTAGGTACATATGCTTGCTTCATTATGGTCATATIS:: ABLATGLYSELUGLYASPATGLEUILEVALALAVALASNSCATASPATGLEUILHIEVALAVALASNSCATASPATGTTATCGTTGCGCTTTCTACTGATGGTGGGATTATCTTATCGTTGCGCTTTCTACTGATGATGATGATGATGATATGATATGATATGATATGATATGAACAACGTAAGGAAGG	Db 193 GAGTCTATTAGATACGTAGATATCTCTGAAGAAGGGACAGAAAGAA 249 Qy 421IlealaGlyIleLeuProAspLeuLeuValLySGlyGlyAspTyrLySProGlu 438 S:	GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Mitchem, Jennifer APPLICANT: Bhatta, Ajay APPLICANT: Bhatta, Ajay APPLICANT: Bhatta, Ajay APPLICANT: Wang, Yanni APPLICANT: Wang, Siqing APPLICANT: Wang, Siqing APPLICANT: Jodes, Mitcheal APPLICANT: Jodes, Mitcheal APPLICANT: Jones, Robert APPLICANT: Jones, Robert APPLICANT: Jones, Robert APPLICANT: Jones, Robert APPLICANT: Barth, Brenda APPLICANT: Carter, Darrick APPLICANT: Darrick APPLICANT: Darrick APPLICANT: Carter, Darrick APPLICANT: Carter, Darrick APPLICANT: Darrick	

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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
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  13059 GTCGTGATGGTCACCCGAGTGGGCAACGATGTGTTCGCCGACACCACGTTGGACAACTTT 13000
                                                                                                                                                                                                                                                                                                      -----CGACAAGACATIGCCACGIGCAAACICATCATGCIGCAG--- 12811
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|12693 GGAATTGAGTTCTTCATGCCGAACGAGTCCGAGCTTGAACTCATAACGGGGATGCCAGTA 12634
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12573 AFCATGGFAACTFTGGGTTGGGTGGGGGCCCACGCAGAAGGAGGAAAATC 12514
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                                                                                                                  LysCysAspPheValSerValProThrHisProThrIleThrLysLeuArgValLeuSer 111
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                                                                                                                                                                                              112 ArgAsnGlnGlnLeuIleArgLeuAspPheGluGluGlyPheGluGlyValAspProGln
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12753 ATCCCAATACTCTCAATCCGGTCGGTCGCACCAGAACTGGATCTTGAGCGAATCGGC
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                                                                          12999 CGCAAAAACGGTATCGATACTACCCATGTTG---CGTACCGATGCGAGCTCCGGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 ThrGluGluGluIleValGluArgGlyMetLysLeuIleAlaAspTyrGluLeuSerAla
                                        -- AspAlaAlaArgAlaLeuSerLysSerLeuAlaAspValAsnVal
                                                                                                                                                                                                                                                                                                                                                152 TyralaLysGlyalaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArgLysAlaGly
                                                                                                                                                                                                                                  12888 GCTAACGCTCAGCTGAGTCCTGCTGATGTCGAGGGTGCC-----
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Zhang, Yanni
Wang, Siqing
Jen, Shyian
Lodes, Michael
Benson, Darin
Jones, Robert
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APPLICANT: Skeiky, Yasir
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Persing, David
Bhatia, Ajay
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Barth, Brenda
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TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 30992
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                                                                                                                  ------ ACTCCGAGGTTCCAG 3539
                                                                                                                                                                                            3540 GAGGTTTTCGACGCCATCCTCGACGAAGTGGTCGTGGACGGAGCCACGATTGCTCACGAG 3599
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3600 GCTCTCGGGCATGAACCGGAATCTTGGGTGAGAAACGGATTGAAGAGGTTCACACGGTC 3659
                        419 ArgLeuIleAlaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysProGlu 438
LysGlyAspSerArgProValAsn------proLeuGluGlnArgMetIleValLeu 400
                                                                                                                                                                                                                                439 GlulleAlaGlySerLysGluValTrpAlaAsnGly-----GlyGluValLeuValLeu 456
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                                                                          GlyAlaLeuGluAlaValAspTrpValValSerPheGluGluAspThrPro--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-912-020-325 (1-477) x PCT-US02-32727-107 (1-21263)
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Matches:
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Persing, David
Bhatia, Ajay
Maisonneuve, Jean Francois
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 107, Application PC/TUS0232727
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer
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                                                                                                                3522 GGA-----
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Benson, Darin
Jones, Robert
Carter, Darrick
Barth, Brenda
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37.75%
24.83%
6.00%
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Wang, Siqing
Jen, Shylan
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Best Local Similarity:
Query Match:
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			uGluArgPro 50 GCGGCGACCG 387	.aArgLeuVal 70 ::: CAGAAT-ATC 446	8	-CTCGAGGAGTTG 497	rsLeuArgVal 109 ::: NTCTTGCGCTG 536	p 12	::: GGTATTCCC 575	aLeu 147	CACCGACTAT 635	16	GICGCCIGIT 695	eAsp	CCTC 747	coAsnLeuSer 197	21	CGCAGCTTTG 807	uGlnGlyMet 237	GGCAGGATGC 867	nGluValTyr 257	GGCTGTC 924	G1y 27))	297	GGTGACCAAG 1044
• • .	Length: 1434 Matches: 102 Conservative: 59 Mismatches: 166 Indels: 20	-176 (1-1434)	ValValLysValAsnThrIleGl :::::: GTCTTGCGGTGGATACGGGCCGC	aSerLeuGlyAlaAsnAlaAr 	gAlaLeuSerLysSerL		rHisProThrIleThrLysLeuArgVal ::: :::	gLeuAspPheGluGluGlyPheGluGlyValAs	 TTCGAAACGGT	aLeuSerSerIleGlyA	CATCCTTGAAGTTGGTG	yAlaLeuAlaServalG	CCAGCTAGCCAAGTTAC	gLysAlaGlyValProV	TCAACTCGGCATTG G	yAlaThrLeuLeuThrP:::	rGluGluGluIleValG	GAGGATGATCCTGACGCAGCTTT	uLeuValThrArgSerG	TGTCATCACCTTGGGAT	.sMetProThrGlnAlaG	GGCTGCGGCGACCGTGA	yValLeuAlaAlaThrL	TGCGTTGGCTGCAGAAC	nAlaAlaAlaGlyValV	CGCGGTGGCGACTTTGA
: 30992 acnes	0.00052 Lengi 140.00 Matci 35.23% Cons 22.32% Mism 5.85% Indei	7) x PCT-US02-32727	valPro ::: cacaccgccrgccc	GlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLeuVal 	GlyLeuThrGlyIleAspAspAlaAlaArgAlaLeu	TCGAGGATTGGCCTTTTCT	<pre>spPheValSerValProThrHi AT</pre>	eAr		ProGlnProLeuHisGluArglleAsnGlnAlaLeuSerSerIleGlyAlaLeu	accaacgagggggggggtgttttaggtgacgccatccttgaagttggtgtcaccgactat	LeuSerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetll.	ACCGGGCGTTTCCGGATAAGCCTGAAGGCCAGCTAGCCAAGTTACGGTCGGCTGTT		CGCTAGGACAGCTGGCAC	SGlyThrAspPheGluArgTyrArgGlyAlaThrLeuLeuThrProAsnLeu :::::::: ::: -ccamcanamacccaacaacaaan	eGluAlaValValGlyLySCySLySThrGluGluGluIleValGluArgGlyMet		LysLeulleAlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGl	CCCCAGCTGTTGAACCTTGGGTGCCGCAGTGTTTTTCATCACCTTGGGATCGGCAGGATGC	erLeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluVal	ATCGTCGGCGGGCCGGAAGGGTTCGACGCCGTGGCGGCGACCGTGAAGGCTGTC	AspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGl	CGGGAGAIGCIIICGIIG	AsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLys	AGGGTTGCCGTTTTGCTAC
NUMBER OF SEQ ID NOS EQ ID NO 176 LENGTH: 1434 TYPE: DNA ORGANISM: Propioni -US02-32727-176	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:						AsnvalLysCysAspPheval: :::::: GGAATCCGGTGTGAT					:	TTGT			ProLy	GluPh				S					5 CGTACTCTTGTCG
; NUMBER O ; SEQ ID NO ; LENGTH: ; TYPE: D ; ORGANIS	Alignment Pred. No. Score: Percent S Best Loca Query Mat DB:	US-09-912	Qy 35 Db 328	Qy 51		Db 447	Qy 90 Db 498	-	Db 537	0y 130	925 da		9E9 qa		969 qa	Oy 178		Db 784	Oy 218	Db 808	Qy 238	Db 868	25	76	27	386 qa

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US-10-092-411A-2746

Sequence 2746, Application US/10092411A.

Sequence 2746, Application US/10092411A.

GENERAL INFORMATION:

TTILE OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 032796-101

CURRENT APPLICATION NUMBER: US/10/092,411A

CURRENT PILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

SEQ ID NO 2746

SEQ ID NO 2746
                                                                                                                                                                                                                                                                                                                                                                                       1209 CCTCATGAGGTCCCGGTGATTGACCTCGCTGTGGTGCTGGGA-------- 1250
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                    ----TGCTTAATCCCCAATTGTGTGCG-GCG 1151
                                                                                                                                                                                                                                                        1152 GTGGCCAGGTTGGGGCACACCCAG-----1175
                                                                                                                                                                                                                                                                                          371 IleValAlaValAsnSerAspAlaSerThrLysArgLeuLysGlyAspSerArgProVal 390
                                                                    315 -----ArgalaaspThrGlyPheGlyValMetThrGluGluGluLeuLysLeu 330
                                                                                                                                              331 AlaValAlaAlaAlaArgLySArgGlyGluLySValValMetThrAsnGlyValPheAsp 350
                                                                                                                                                                                                                      351 IleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeu 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 ProAspLeuLeuValLysGlyGlyAspTyrLysProGluGluIleAlaGlySerLysGlu 445
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                                                                                                                                                                                                                                                                                                                                                                    391 Asn-----ProLeuGluGlnArgMetIleValLeuGlyAlaLeuGluAlaValAsp 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                            408 TrpValValSerPheGluGluAspThrPro-----GlnArgLeuIleAlaGlyIleLeu
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                              137.50
43.28%
21.64%
5.75%
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Best Local Similarity:
Query Match:
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; CURRENT FILING DATE: 2002-10-11 ; NUMBER OF SEQ ID NOS: 30992 ; SEQ ID NO 132 ; LENGTH: 13380 ; TYPE: DNA ; ORGANISM: Propioni acnes PCT-US02-32727-132	Alignment Scores: 0.0449 Length: 13380 Pred. No.: 133.00 Matches: 124 Score: 34.96% Conservative: 69 Best Local Similarity: 22.46% Mismatches: 183 Query Match: 15.56% Indels: 177 DB: 27	US-09-912-020-325 (1-477) x PCT-US02-32727-132 (1-13380) Qy 13 ValMetValValGlyAspValMetLeuAspArgTyrTrplycGlyProThrSer 30	31 ArgileSerProGluAlaProValProValValLysValAsnThrileGluGluArgPro	70 ValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSGrLeuAlaAspVal 10 ValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSGrLeuAlaAspVal 11 11 11 11 11 11 11 11 11 11 11 11 11	Oy 90 AsnValLysCysAspPheValSerVal	Db 8719 GAGATCTTTCCTCCCGACGACTTCCCGCTCTTCTACCGGCGTCTTACCCAGAT 8778 Qy 107 LeuargValleuSerArgAsnGlnGlnLeuIlearg 118	Oy 119 LeuaspPheGluGluGlyPheGluGlyvalaspProGlnProLeuHisGluarglleasn 138	### ##################################	175 LeulleAspProLysGlyThrAspPheGluArgTyrArgGlyAlaThrLeuLeuThrPro 	Qy 195 AsnLeuSerGluPheGlualaValValGlyLysCysLysThrGluGluGlu 211	Qy 212 IleValGluArgGlyMetLysLeuIleAlaAspTyrGluLguSerAlaLeuLeu 229 :::::::: :::::	Qy 230 ValThrArgserGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisMet 249 :::
Oy 71 GlyLeuThrGlyIleAspAsPalaAlaArgAlaLeuSerLySSerLeuAlaAspValAsn 90	Qy 111 SerArgAsnGlnGlnLeuIleargLeuAspPheGluGluGlyPheGluGlyValAspPro 130	Oy 145 GlyAlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGln 162	Db 457 ATAGCACAAATCACTGAAAAACTGGTGCGCAACTAGTTGTTGATGCAGAAAAAGATCTT 516 Qy 183 PheGluargTyrargGlyalaThrLeuLeuThrProAsnLeuSerGluPhe 199	20 CALLINGTON AND STATEMENT CONTROLL CONTROLL OF STATEMENTS 21 [1]	Db 634 ATTTGAAAAAGGGCACAATCAGTCATCATTGACTTGGTGGCGATGGTGCAATATAT 693 Qy 239 LeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGln 254 :::	Oy 255 GluvalTyrAspvalThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeu 274	Db 796 TCCATGGTCTTATAGATGAAGGTTTTCAACAGGCGTAGCTTCA 843 Qy 295 ValG1yLysLeuG1yThrSerThr 302 Db 844GGAACAGCGACT 855	RESULT 9 PCT-US02-32727-132 Sequence 132, Application PC/TUS0232727 GENERAL INFORMATION: APPLICANT: MITCHAM, Jennifer	Persing Persin	; APPLICANT: Wang, Siqing ; APPLICANT: Jen, Shyian ; APPLICANT: Lodes, Michael ; APPLICANT: Benson, Darin	; APPLICANT: Jones, Robert ; APPLICANT: Carter, Darrick ; APPLICANT: Branda ; APPLICANT: Bronda	INV REN

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Sequence 1139, Application US/09134000C
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFREENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1139
LENGTH: 432
                    9396 GCATCTGTCATGACGCGCACCCCGCTTATTGACAAGCTGTTAGATCGGCGACTTGCCGAT 9455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----CTCGCAGCGGGAGGTCGTGCCGATGCCATGGCTGACCGGGAACACCTC 9605
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                                                                                                                                                                                                                                                                                                                                                                                                                                    9456 CCGGTGCGTTTTGCCGATCGCGTCCCGCAGCGTCCCCGAGCGACGTGGAGCCCCACTGAA 9515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9516 ccgcrcarcgrcgrcgccgcrgarcarccrgcrcgcggrgca------9557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 GluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysValValMetThrAsn 346
                                                                                                                                                          287 AlaAsnAlaAlaAlaGlyValValValGlyLysLeuGlyThrSerThrValSerProIle 306
                                                                                                                                                                                                                                      307 GluLeuGluAsnAlaValArgGlyArgAlaAspThr-------Gly 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 GlyAspArgLeuIleValAla-------ValAsnSerAspAlaSerThrLys 381
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ProThrGlnAlaGlnGluValTyrAspValThr-----GlyAlaGlyAspThrVal 266
                                                                                                                                                                                 267 IleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9777 ACGGGTACGACGTGCAAGGAATCCTT---------
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US-09-134-000C-1139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   439 GluIleAlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeuAsnPhe 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        328 TTTGATTTTCTAGAAGTTGAAACAACCGCA-----AAGGTTCTTTATTTGCCACGA 378
                                                                                                                                                                                                                                                                                                                    96
                                                                                                                                                                                                                                                                                                        361 AlaAsnAlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThr
                                                                                                                                                                                                                                                                                                                                                                                                                                           381 LysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMetIleValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 TTAGAAAAAAGAAACAAAGT-----TATTTTTCATATGAAAAAGGTAAACAATTATTA
                                                                                                                                                                                                                                                                                 341 LysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeu
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GENERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INVENTION:

FILE REFERENCE: PA131P1

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2001-05-18

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEO ID NOS: 2876
                                                                                                                                                                                                                                           US-09-912-020-325 (1-477) x US-09-134-000C-1139 (1-432)
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                                                                                                                                         Conservative:
Mismatches:
                                                                                                                         Matches:
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LOCATION: (919)..(919)
OTHER INFORMATION: n equals a,t,g, or
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; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000c-1139
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LOCATION: (895)..(895)
OTHER INFORMATION: n equals
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LOCATION: (910)..(910)
OTHER INFORMATION: n equals
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                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                 Alignment Scores:
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LENGTH: 962
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156 AlaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArgLysAlaGlyValProValLeu 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 ATTGTCATA------GTGGCTGGAGCAAATTTACTTTTGAATACGGAGGAT 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 CTGAGGGCAGCAGCAATGTCATTAGCAGACCAAAGTCATGGTCTGCCAGCTCGAAATA 529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 ACTICICGITIGCCAAAACIGGA-------GAAACCAICCAIGGA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 CATAAGTITITIATIGGCTITIGGAGGGAAAGGIGCCAACCAGTGIGTCCAAGCIGCICGG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 SerLysSerLeuAlaAspValAsnValLysCysAspPheValSerValProThrHisPro 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 IleAspPro-----LysGlyThrAspPheGluArgTyrArgGlyAlaThrLeu 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluArgAlaGlyValMetValValGlyAspValMetLeuAspArgTyrTrpTyrGlyPro
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Matches:
Conservative:
Mismatches:
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LOCATION: (960)..(960)
OTHER INFORMATION: n equals a,t,g, or
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              LOCATION: (952)...(952)
OTHER INFORMATION: n equals a,t,g,
FEATURE:
MAME/KEY: misc_feature
LOCATION: (954)...(954)
OTHER INFORMATION: n equals a,t,g,
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24.578
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APPLICANT: Carter, Darrick
APPLICANT: Barth, Brenda
APPLICANT: Douglass, John
TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
FILE REFERENCE: 210121.514C1
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT APPLICATION NUMBER: PCT/US02/32727
CURRENT FILING DATE: 2002-10-11
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                                                                  4 ThrLeuProGluPheGluArgAlaGlyValMetValValGlyAspValMetLeuAspArg
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                                               243 GlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGlyAla
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Matches:
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Persing, David
Bhatia, Ajay
Maisonneuve, Jean Francois
Zhang, Yanni
Wang, Siqing
Jen, Shyian
                                                                                                                263 GlyAspThrValIleGlyValLeuAla 271
                                                                                                                                     Sequence 16, Application PC/TUS0232727 GENERAL INFORMATION:
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APPLICANT: Skeikv, Yasir
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Benson, Darin
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ORGANISM: Propioni acnes
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LENGTH: 61557
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Oy 372 ValAlaValAsn Db 33567 GTGGCGGTCAATGGGCTCG Qy 376 SerAspalaSerThrLysA Qy 376 ArghetileValLeuGlyA Qy 396 ArghetileValLeuGlyA Db 33687 GGTGGTCATCGCTCGACG	RESULT 13 US-09-134-000C-1809 Sequence 1809, Application GENERAL INFORMATION: APPLICANT: Lynn boucette-S TITLE OF INVENTION: NUCLEI TITLE OF INVENTION: ENTER	CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 1998 PRIOR APPLICATION NUMBER: PRIOR PILING DATE: 1997-08 NUMBER OF SEQ ID NOS: 6812 SEQ ID NO 1809 LENGTH: 810	; TYPE: DNA ; ORGANISM: Enterococcus fa US-09-134-000C-1809 Alignment Scores: Pred. No.: Score: Percent Similarity: 44.59	Best Local Similarity: 25.68 Query Match: 5.048 DB: 5.048 US-09-912-020-325 (1-477) x U QY 184 GluargTyrArgGlyAlaT	361 GAGGGGGGGTCC 191	Db 481 ATTAAATCACAGATGAAG QY 225 LeuSeralaLeuLeuValT :: :::::: Db 541 ATTGAAGCAGTAATTATTA QY 245 AlaProLeuHisMetProT ::: ::!		Db 778 ATTCCTTATCAACACGAAT
Qy 120		183 PheGluArgTyrArgGlyAlaThrLeuleuThrProAsnLeu 196 :::::::	217 MetLys	249	279 SerLeuGluGluAlaCysPhe		330	
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SArgLeuLysGlyAspSerArgProValAsnProLeuGluGln 395
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scGCCGCCAGGAGTCCACTCCGCTGCCGTGCAGAA 33686
                   SGACGAGCGCGCATCGACCCTGCCATCGTCTTCTTGGAAGCG 33626
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|AGGTCAAATCCCGCACCTGCGTTAGAACAAGTTCCTGAAGAA 420
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AGTAGTATTAGAAAAAGATTTTAGCAATTTGGAAGAAGCT 717
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Matches:
Conservative:
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Indels:
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GCCGTT 33710
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6770 TACTGGGTTTGGGGGAAGCC 6751
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                                                                                                           materials incorporating
                                      JUNEARLY INFORMATION:

APPLICANT: Havukkala, Ilkka J
APPLICANT: Lubbers, Mark William
APPLICANT: Dekker, James
TITLE OF INVENTION: Polynucleotides, materials incorpora;
TITLE OF INVENTION: them, and methods for using them.;
FILE REPERENCE: 11000.1043 c3
CURRENT APPLICATION NUMBER: US/10/264,213
CURRENT FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 12023
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Matches:.
            Sequence 100, Application US/10264213 GENERAL INFORMATION:
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7358 TGCCCAGCGTGCAGATGTGATTATTGGCACGCGTGACGAATTTGATGTTCTGGAAAATCA 7299
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6890 CAGTICGATIGACAACCGCGCAGCCCTCGTGCGCTTTTTAAACCAACAATATCTTGATG 6831
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                                                                                                                                                                                                             -LysCysLysThrGluGluGluIleValGluArgGlyMetLysLeuIleAlaAspTyrGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 sAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGlyAlaGlyAs
                                                                                     ----ArgGiyAlaThrLeuLeuThrProAsnLeuSerGluPheGluAlaValValGly--
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TITLE OF INVENTION: Variants of alternative
FILE REPERENCE: 1291B1.4 Compugen
CURRENT APPLICATION NUMBER: 08/09/724,676
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PATENTIN version 3.2
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; Sequence 45787, Application US/09724676
; GENERAL INFORMATION:
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165 185 185 230 205	216 216 308 236 368	252 428 272 470	292 530 312 545	331 605 348 665 368 725	38 78 39 84 41	209 209
AlaLeuValLeuSerAspTyrAlaLysGlyAlaLeuAlaSerValG	206 CyslysThrGluGluGluIleVal	237 MetSerLeuLeuGlnProGlyLysalaProLeuHisMetProThrGln :::	273 ThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaGly	313 ArgGlyArgAlaAspThrGlyPheGlyValMetThrGluGluGluLeuLysLeuAla	369 ArgLeulleValAlasnSerAspAlaSerThrLysArgLeuLysGlyAsp	846 TCAGAAGTGGTGATGGAGCCCCGTACGCGGTCACAGCAGAGCTCCTAAGTCACTTCAAG 414 GluaspThrProGlnargLeuIleAlaGlyIleLeuProAsp 427 111 906 GTGGACCTGGTGTCACGGCAAGAAATTATCCCTGAC 947
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Search completed: November 27, 2002, 02:55:41 Job time: 165 secs

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AX188888 Sequence
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U01777 Mycoplasma
AF186316 Echinomet
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AX341713 Sequence
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AR128860
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AX119171
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-Q-CQ012_1/102FO_spool/JUG9912020/runat_20112002_150259_11086/app_query.fasta_1.647
-Q-CQ012_1/102FO_spool/JUG9912020/runat_20112002_150259_11086/app_query.fasta_1.647
-Q012_1/102FO_spool/JUG9912020/runat_201300.rge -WINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=-pct -THR_MAX=100 -THR_MIN=0 -ALDN=1.50
-UOSE-LCGAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-300
-USER-US09912020_@CGN_1 1_3637_@runat_20112002_150259_11086 -NCPU=6 -ICPU-3
-NO.MARP -LARGEOURRY -NGC_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                       November 24, 2002, 23:18:35; Search time 3218 Seconds (without alignments) 4313.871 Million cell updates/sec
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1 MKVTLPEFERAGVMVVGDVM.....FEDGCSTINIIKKIQQDKKG
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                             OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 300
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                                                                                                                                                                                                                                                                                                                                                                       327 GluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysValValMetThrAsn 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230
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                                                                                             1 (bases 1 to 294)
Mahan,M.J., Conner,C.P. and Heithoff,D.M.
Method and probes for the identification of microbial genes specifically induced during host infection
Patent: US 6365401.A 186 02-APR-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            177 GAGTTGAGACAGGCCGTCGCCAGCGCGTAAGTC----GCGAGAAGTGTCATGACCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 GlyValPheAspIle---LeuHis-----AlaGlyHisValSerTyrLeu 360
            PAT
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Human polynucleotides and polypeptides encoded thereby
Patent: Wo 0190366-A 4327 29-NOV-2001;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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      294 bp Dl Sequence 186 from patent US 6365401.
AR203747
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/db_xref="taxon:9606"
68 c 83 g 41
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73 c 96 g
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AX311342
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AR203747
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/translation="PEAPVQVVDVKDENNRLGGACNVVHNLIALNAQVFVCGVVGNDE AGFWLGEKLESMGVDISYLFVDTSRPTTKKTRVIIANQQVLRVDRES" 41 c 71 g 86 t
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/protein_id="AAL16695.1"
/db_xref="GI:16265978"
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Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library and sequence analysis of the selected genomic regions Unpublished
2 (bases 1 to 273)
6 (bases 1 to 273)
6 (bases 1 to 273)
7 Eng.Y. and Fox.J.G.
Direct Submission
Submitted (09-MAR-2001) Division of Comparative Medicine,
Massachusetts Institute of Technology, 77 Massachusetts Avenue,
Cambridge, MA 02139, USA
1 273
                                                                                                                                                                                                                                                                     61 GCGTTATGGCGAGCATTAAGGGCGTGGCGATGTTTTTCGACGAGATACGCCG 120
                                                                                                                                                                                                                                                   417
                                                                                                                                                                                                                                                                                                                                              121 ATCGAGCTCCTGCGCGCGCTCTCGCCGGACGTCAAGGGAGCCGACTATCGAGAA 180
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        .7organism="Helicobacter hepaticus" /strain="3B1; ATCC 51449" /db_xref="ATCC:51449"

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                       Matches:
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 Length:
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Ge,Z., Feng,Y. and Fox,J.G.
Helicobacter hepaticus genome:
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/transl_table=11
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Helicobacter hepaticus
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/gene="rfaE"
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Peterson, S.N.
Direct Submission
Submitted (13-SEP-1993) Peterson S.N., University of North Carolina Medical School, Microbiology and Immunology, Chapel Hill, NC 27599
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                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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Mycoplasma genitalium
Mycoplasma genitalium
Bacteria; Firmicutes; Mollicutes; Mycoplasma.
i (sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Characterization and analysis of the Mycoplasma genitalium Thesis (1992) Microbiology and Immunology, University of No Carolina Medical School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 ---AlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAiaAlaAlaGlyValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 TACCCAAGTCTGTCCTTGGAAGAATGCTCAAGAGATCTAATTCCATCGCTGCGGTCAGC
                                                                                                        Mendrick,D., Porter,M.W., Johnson,K.R., Castle,A.L. and Elashoff,M.R. Molecular toxicology modeling Patent: WO 0210453-A 1264 07-FEB-2002; Gene Logic, Inc. (US)
                                                                                                                                                                                                             /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/note="EMBL/GenBank Accession No. A1236089"
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                                                   Chordata;
Rodentia;
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                                     Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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MGU01777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
1 (Joses 1 to 272)
Forsyth, R.A., Ohlsen, K.L. and Zyskind, J.W.
Forsyth, R.A., Ohlsen, K.L. and Zyskind, J.W.
Genes identified as required for proliferation of E. coli
Patent: Wo 0148209-A 89 C5-JUL-2001;
Elitra Pharmaceuticals, Inc. (US)
                                                                                                                                                                      181 TCTTATCTTTTTGTAGATACTTCGCGTCCTACGACTAAAAAACGCGTGTTATCATTGCT 240
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                                                                                            34 ProGlualaProvalProvalValLysValAsnThrIleGluGluArgProGlyGlyAla
                                                                                                                                                                                                                                                                     94 AspPheValSerValProThr --- HisProThrIleThrLysLeuArgValLeuSerArg
                                                                                                                                                     54 AlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLeuValGlyLeuThr
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Mismatches:
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/organism="Escherichia coli"
/db_xref="taxon:562"
a 61 c 61 g 85 t
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Sequence 1264 from Patent WO0210453.
AX401588 1 GI:21337768
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 89 from Patent W00148209. AX188888
                                                               US-09-912-020-325 (1-477) x AF358705 (1-273)
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INV 10-NOV-1999
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Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
Location/Qualifiers
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Echinometra mathaei isolate Flc.10 bindin precursor, gene, partial
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Echinometra mathaei
Echinometra mathaei
Eukaryota; Metazaa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinoea; Echinoida; Echinometridae;
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/db_xref="taxon:31178"
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Palumbi,S.R.
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Palumb1, S.R.
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Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
Location/Qualifiers
1. 300
/organism="Echinometra mathaei"
/isolate="Flc.7"
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Echinometra mathaei isolate F1c.7 bindin precursor, gene, partial
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Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
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18
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                                           /organism="Mycoplasma genitalium"
/isolate="G-37"
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Matches:
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                                                                     /db_xref="taxon:2097"
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<2. .>264
               Location/Qualifiers
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AF186316.1 GI:6318982
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Echinometra mathaei
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Palumbi,S.R.
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Palumbi, S.R.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
1 (bases 1 to 245)
Forsyth.R.A., Ohlsen,K.L. and Zyskind,J.W.
Foresyth.R.A. 901Sen,K.L. and Zyskind,J.W.
Patent: WO 0148209-A 90 05-JUL-2001;
Elitra Pharmaceuticals, Inc. (US)
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/db_xref="taxon:562"
53 c 55 g 80 t
                                             sp.
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Honolulu, HI 96822, USA
Location/Qualifiers
1. 300
/organism="Echinometra
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                                                                                                                               /translation="YGNYPQARNPPWGGGNYPVPGQAPMGQLAQQGYAAPGMGGPVGG
GGGAMAGPFGGGAGPVGGGGAGPPEFGEMPEAEGAEEEGDKDYSSVDEEETTISAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INV 21-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 300)
Metz,E.C. and Palumbi,S.R.
Mositive selection and sequence rearrangements generate extensive
polymorphism in the gamete recognition protein bindin
Mol. Biol. Evol. 13 (2), 397-406 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Echinometra sp.
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 300)
Metz.E. and Palumbl,S.R.
Direct Submission
Submitted (26-OCT-1995) Edward C. Metz, Zoology, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 -------GGTGGTGCAATGGCCGGGCCTTTCGGTGGGGGAGCTGGGCCTGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336
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                                                                                                                                                                                                                                                                                                                                                                                       262 AlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGlu 281
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110
331
4
                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:

    .300
    /organism="Echinometra mathaei"

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                                                                     /codon_start=1
/product="bindin precursor"
/protein_id="AAF07131.1"
/db_xref="G1:6319068"
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                                                                                                                                                                                                                                                                                                                                             (1-300)
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                           /isolate="Flc.10"
/db_xref="taxon:31178"
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/product="bindin"
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72.00
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30.84%
3.01%
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U39543.1 GI:1122528
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Best Local Similarity:
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DB:
   source
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TITLE
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ESU39543
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/product="bindin precursor"
/protein_id="AAR07091.1"
/d_xref="G1:6319028"
/translation="KGNYPQARNPPWGGGNYPVPGQAPMGGLAQOGYAAPGMGGPVGG
GGGAMAGPIGGGAGPVGGGGGGGAGPPEFGEMPEEGDKDYSSYDEEETISAK"
                                                                                                                                                                                                                                                                                                                        AF186277 285 bp · DNA linear INV 10-NOV-1999
Echinometra mathaei isolate Guam3.1 bindin precursor, gene, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Echinodermata; Elèutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
                                                          -----ATGAGGACTACAGTAGC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  All males are not created equal: fertility differences depend gamete recognition polymorphisms in sea urchins Proc. Natl. Acad. Sci. U.S.A. 96 (22), 12632-12637 (1999) 20006286
                                                                                                      301 rThrValSerProIleGluLeuGluAsn--------AlaValAr
                                                                                                                                                                    313 gGlyArgAlaAspThrGlyPheGlyValMetThrGluGluGluLeuLysLeuAlaValAl
                                         GluAlaCysPhePheAlaAsnAlaAlaAlaGlyValVal-ValGlyLySLeuGlyThrSe
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Mismatches:
Indels:

    .285
    /organism="Echinometra mathaei"
/isolate="Guam3.1"

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Matches:
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/product="bindin"
a 66 c 104
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AF186277.1 GI:6318943
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Echinometra mathaei.
Echinometra mathaei
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1 (bases 1 to 285)
Palumbi, S.R.
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Palumbi, S.R.
              112 ATGGTGGACCGGTCGGTGGT
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39.22%
29.41%
2.90%
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Query Match:
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ORIGIN
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VERSION
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AUTHORS
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/protein_id="AAF07095.1"
/brotein_id="AAF07095.1"
/db_xxef="c1:6319032"
/translation="YGNYPORNPPWGGGTYPVPGQAPMGOLAQOGYAAPGMGGPVGGGGAAMAGPIGGGAGPVGGGGAGPPEFGGMSEEBGAEGEGDEDYSSTGEEETISAK"
                                                                                                                                                                                                                                                                           AF186281 300 bp DNA linear INV 10-NOV-1999 Echinometra mathaei isolate Guam5.1 bindin precursor, gene, partial
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Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
Location/Qualifiers
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Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
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111
239
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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                                            Length:
Matches:
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                                                                                                                                                    (1-245)
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/db_xref="taxon:31178"
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69 c 113
                                                                                                                                                    US-09-912-020-325 (1-477) x AX188889
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AF186281
AF186281.1 GI:6318947
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70.00
38.18%
28.18%
2.93%
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70.00
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Echinometra mathaei
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Palumbi, S.R.
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Palumbi, S.R.
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
                              Alignment Scores:
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                                            I. NO.:
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TITLE
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AUTHORS
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242 ProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGly 261
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Echinometra mathaei
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Palumbi, S.R.
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Palumbi, S.R.
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Echinometra
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AUTHORS
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AF186282
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GGGAMAGPIGGGAGPVGGGGAGPPEFGEMPEEEGDKDYSSVDEEETTISAK"
                                                                                                                                                                                                                                                                                                                                    AF186279 285 bp DNA linear INV 10-NOV-1999
Echinometra mathael isolate Guam4.1 bindin precursor, gene, partial
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Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
Location/Qualifiers
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Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
                                                                                                                                       321
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                                                                                                                                                                                                            218 -TGCCCGAAGAGGAGGGTGATAAGGACTACAGTAGCGTCGATGAGGAAGAGACAACAATT 276
                                                                                 301
CCCGGTCAAGCACCT----ATGGGTCAGCTAGCCCAACAAGGTTACGCTGCTCCTGGA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              All males are not created equal: fertility differences depend gamete recognition polymorphisms in sea urchins Proc. Natl. Acad. Sci. U.S.A. 96 (22), 12632-12637 (1999) 20006286
                           262 AlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGlu 281
                                                                               282 GlualaCysPhePheAlaAsnAlaAlaGlyValVal-ValGlyLysLeuGlyThrSe
                                                                                                                                     301 rThrvalSerProIleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPheGl
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Matches:
Conservative:
Mismatches:

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    /organism="Echinometra mathaei"

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                                                     112 ATGGGTGGACCGGTCGTGGT------
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66 c 104
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AF186279.1 GI:6318945
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39.22%
29.41%
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Echinometra mathaei
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Palumbi, S.R.
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Palumbi,S.R.
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Best Local Similarity:
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 28
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AF186279
LOCUS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 bp DNA linear INV 10-NOV-1999 mathaei isolate Guam5.2 bindin precursor, gene, partial
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Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         All males are not created equal: fertility differences depend on gamete recognition polymorphisms in sea urchins Proc. Natl. Acad. Sci. U.S.A. 96 (22), 12632-12637 (1999) 20006286
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Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
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262 AlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGlu 281
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                                                                                                                                                                                                                                                              301 rThrValSerProIleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPheGl 321
                                                                                                                                                               282 GluAlaCysPhePheAlaAsnAlaAlaAlaGlyValVal-ValGlyLysLeuGlyThrSe
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Mismatches:
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GGGAIAGPIGRGAGPVGGGGAGPPEFGEMPEEEGDKDYSSVDEEETTISAK"
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Echinometra mathael isolate Guam7.1 bindin precursor, gene, partial
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Submitted (14-SEP-1999) Organismic & Evolutionary Biology, Harvard
University, 16 Divinity Ave., Cambridge, MA 02138, USA
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinosea; Echinoida; Echinometridae;
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                                                                                                                                                                                                                     133 ------GGTGGTGGTGCAATGCCCGGGCCTATCGGTGGGGGAGCTGGGCCTGTC 180
                                                                                  282 GluAlaCysPhePheAlaAsnAlaAlaAlaGlyValVal-ValGlyLysLeuGlyThrSe 301
                                                                                                                                                                                                                                                                                                                                  321 yValMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLy 341 :::: | | | | | | | | | | :::
                                                                242 ProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGly 261
                                                                                                                                 262 AlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGlu 281
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    /organism="Echinometra mathaei"

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                               US-09-912-020-325 (1-477) x AF186282 (1-285)
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                                                                                                                                                               112 ATGGGTGGACCGGTCGGTGGT-----
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67 c 102
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AF186284.1 GI:6318950
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Palumbi, S.R.
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Palumbi, S.R.
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Indels:
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                                                                                                                              US-09-912-020-325 (1-477) x AF186284 (1-285)
                                                                                                                                                                                                                                                                                                               112 ATGGGTGGACCGGTCGTCT------
                                                                                      Gaps:
           39.22%
29.41%
2.90%
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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SUMMARIES

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-DB-#Geneseq_101002 - OFWHT-fastap - SUFFIX-plaszlm300.rng - WINNATCH-0.1
-TRANS-human40.cd1 - LIST-45 - DOCALION-200 - THR_SCORE-pct - THR_MAX=100
-THR_MIN-0 - ALIGN-15 - MODE-LOCAL - OUTFMN=pto - NORM-ext - HEAPSIZE-500 - MINLEN-0
-MAXLEN-300 - USER-WISO99120.02.eCGN_11_1_281_ernnat_20112002_150529_11075 - NCPU-6
-DEV_INNEOUT-120 - WARAP - LARGEQUERY - NEG_SCORES-0 - WAIT - LONGLOG
-DEV_INNEOUT-120 - WARN_TIMEOUT-30 - THREADS-1 - XGAPOP-10 - XGAPEXT-0.5 - FGAPOP-6
-FGAPEXT-7 - YGAPOP-10 - YGAPEXT-0.5 - DELOP-6 - DELEXT-7
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3653.752 Million cell updates/sec
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                  OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2185239 segs, 1125999159 residues
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Listing first 45 summaries
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Maximum DB seq length: 300
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Perfect score:
Sequence:
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Pred. No. is the number of results.predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	ult No.	Score	Query Match	Length	DB	DI	Description	
	Н.	7		243	24	ABN77217	uman ORF216	4 CDN
	~ ~	o c		249	18	AAT67445	. pylori cy	topla
U t	m <	7 -		272	77	AAH81290	(coll n
ບ	ֆ Մ			282	7 7	ABL 75687	r sequence rn tassel-	ع د
	9	84.		300	71	AAA67292	lyptus q	randis
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	11	65.5		279	21	ABQ63223	Mycobacterium	lum bovi
	12	9		237	22	AAH52260	Human AFP pro	protein
	13	64		275	74	ABL38371	Human colon t	tumour
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O	17	63.5		267	22	AAI49702	Probe #18388	nsed
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	13	۳,	•	284	23	AAS86615	DNA encoding novel	novel
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c	22	62		149	21	AAA14524	Oligonucleoti	ide 3'
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כ	7 8 7	9 6		283	22	ABA12944	Human nervous	s syst
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	31	61	•	176	74	ABL63015	Breast cancer	r rela
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ر	34	٥.		234	24	ABK80352	Bacillus clausii	usii g
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ပ	3.0	Λσ	•	297	3 6	AAS54270	Pseudomonas a	apriidí
U	300	, ro		117	22	ABA71890	uman foetal	1100
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ΧŁ	08	-,TIII,-200	7	irst entr	<u> </u>	•••		
X	3	1	•		17.	•••		
DE	Human	ORF2	164 cDNA,	A, SEQ	Z CI	NO:4327.		
K	Ξ	in; ORF;	; open	ea		frame; ORFX; drug screen	ing; diagnosis;	
X X	о	ne mod	isease monitoring mmune modulation:	g; cyto ; haema	cytokine; aematopoi	٦ ٢	<pre>10n; cell different1 tissue growth;</pre>	ation;
ΚW		œ	is; activin	ivin; inhibin; c	Inhib	hemotac	chemokinetic; haemosta	tic;
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ΚW	نټ	ue growth		order;	tiss		disorder; diabetes	itus;

Gaps:

24

DB:

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Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-SABN75054 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 80% identical to the ORF2 nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of screening for modulators of ORFX expression or cellulative, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cellulation, immune modulation, haematopoiesis regulation, cellus activity, themostatic activity, themostatic activity, themostatic activity, themostatic activity, themostatic activity, themostatic activity, the creeptor/ligand, antinfilammatory activity, tumour inhibition activity, receptor/ligand, antinfilammatory activity, tumour inhibition activity, and many also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, other proliferative disorders such as psoriasis and benign tumours, other proliferative disorders such as psoriasis and benign tumours, other proliferative disorders such as psoriasis and benign tumours, and any decombined the contents.
                                              vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antihyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
hypothyroidism; cholesterol ester storage disease; infection; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurological disorders such as epilepsy and Alzheimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1338; 2508pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-2001; 2001WO-US17076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-2000; 2000US-206690P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shimkets RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-106200/14.
P-PSDB; ABP33191.
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200190366-A2,
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-NOV-2001.
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cardiovascular diseases, immune system disorders disorders related to organ transplantation, disorders of tissue growth and regeneration, disorders of tissue growth and regeneration, disoraces such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and clouing of homologous sequences, in genetic diagnosis, and forestic diagnosis which may be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX which may be useful for studying the function and/or activity of ORFX which may be useful for studying the function and/or activity of ORFX which may be useful for studying the function and/or activity of ORFX which may be useful for studying the function and/or activity of ORFX which may be useful for studying the function and/or activity of ORFX which may be useful for studying the function and/or activity of ORFX which may be useful for studying the function and or activity of ORFX which may be useful for studying the function and or activity of ORFX which may be useful for studying the function and or activity of ORFX which may be useful for studying the function and or activity of ORFX which may be useful for studying the function and or activity of ORFX was activity of ORFX which may be useful for studying the function and or activity of ORFX was activity of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases.
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Matches:
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Indels:

170.00 65.82% 40.51% 7.10%

Best Local Similarity:

Query Match:

Percent Similarity:

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This sequence encodes a H. pylori cytoplasmic protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino
                                                                                                    417
                                                                                                                                                                                              121 ATCGAGCTCCTGCGCGCCTCTCGCGGACGTGATCGTCAAGGGAGCCGACTATCGAGAA 180
                                   378 AlaSerThrLysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArgMet 397
                                                                                                                                      61 GCCGTTATGGCGAGCATTAAGGGCGTGGCGATGGTCACGTTTTTTCGACGAGATACGCCG 120
                                                                                                                                                                         418 GlnArgLeuIleAlaGlyIleLeuProAspLeuLeuValLysGlyGlyAspTyrLysPro 437
                                                     Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; ds.
                                                                                                                                                                                                                                             GluGluIleAlaGlySerLysGluValTrpAlaAsnGlyGlyGluValLeuValLeu 456
                                                                                                                                                                                                                                                                             181 GACCAAGTGGTCGGCGCCGACCTTGTGAAAACACGGAGGCAGGGTGCTACTTGTG 237
                                                                                                    398 IleValLeuGlyAlaLeuGluAlaValAspTrpValValSerPheGluGluAspThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. pylori cytoplasmic protein ORF 21742157.aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "no stop codon given"
US-09-912-020-325 (1-477) x ABN77217 (1-243)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 176; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                AAT67445 standard; DNA; 249 BP
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95US-0487032
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P-PSDB; AAW20221.
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The present invention describes a purified or isolated nucleic acid asquence (1) consisting essentially of one of the 93 nucleotide sequences given in AAH81202 to AAH81294, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism.
acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                      178 CGTTTGATAGAATTTGAAGAGGTTATTCCACAAGGCGCTATCATAGAAAAAATTAAAAGG 237
                                                                                                                                                                                                                                                                                                                                 GluAspThrProGlnArgLeuIleAlaGlyIleLeuProAspLeuLeuValLysGlyGly 433
                                                                                                                                                                                                                                                                                                                                                                                            AspTyrLysProGluGluIleAlaGlySerLysGluValTrpAlaAsnGlyGlyGluVal 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                   454 LeuValLeuAsnPheGluAspGlyCysSerThrThrAsnIleIleLysLysIleGlnGln 473
                                                                                                                                                                                                                                                                                                  10 AAAGACAGGGCGTTTCTTTTAGCGAGCTTGTCTTGCGTGGATTAJGTTGTGGTGTTTGGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids encoding proteins required for Escherichia coli
proliferation, useful for screening for antimicrobial agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli; identification; proliferation; microorganism; antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis; bacterial growth inhibition; ds.
                                                                                                                                     249
35
17
24
4
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                                                                                        84 A; 39 C; 62 G; 64 T; 0 other;
                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPI; 2001-457376/49.
                                                                                                                                                                               Best Local Similarity:
                                                                                        Sequence 249 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
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                                                                                                                                                                  Percent Similarity
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                                                                                                                     Alignment Scores:
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(I) have antibacterial and antiblotic activities, and can be used in of the microganism inhibits proliferation of the microcranism and the manufactured antiblotic is useful for reducing the activity or level of a gene product required for proliferation of a microcranism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or poliferation can be used as antisense therapeutics for Killing bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as its sequences and provided acid probes complementary to proliferation-required sequences that are specific for particular species of microcranisms can sequences that are specific for particular species of microcranisms can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat sequence differentially expressed in response to a hepatotoxin #1264.
                                                                                                                                                                                                                      represent oligonucleotides, which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  be used as probes to identify particular microorganism species in
clinical specimens. AAH81295 to AAH81487 encode the Escherichia coli
proteins given in AAG98239 to AAG98431, and AAH81488 to AAH81491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening; differential expression; centrilobular necrosis; steatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elashoff MR;
                                                                                                                                                                                                                                                                                                               272
23
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                                                                                                                                                                                                                                                                 61 G; 85 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Castle AL,
                                                                                                                                                                                                                                                                                                                             Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                             Indels:
                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-912-020-325 (1-477) x AAH81290 (1-272)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357/c
ABK63357 standard; cDNA; 292 BP.
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2001US-292336P.
2001US-295798P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001US-297457P.
2001US-298884P.
2001US-303459P.
                                                                                                                                                                                                                                                                 Sequence 272 BP; 65 A; 61 C;
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2001US-290029P
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120.00
100.00%
100.00%
5.01%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENE LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-241625/29
                                                                                                                                                                                                                                       present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             475 LysLysGly 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211 AAAAAAGGC 203
                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200210453-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-NOV-2000;
11-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-2001;
                                                                                                                                                                                                                                                                                               Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK63357;
                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABK63357,
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       8×8666666666666666688×8
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Predicting toxic effects of compounds or the progression of these toxic effects by determining the changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells.

Claim 1; Seq ID No 1264; 239pp; English.

The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the compounds or the progression of these toxic effects by determining the comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic ceffect, preferably the hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The method can also be used to identify an agent which modulates the toxic response and predict cellular pathways that a compound modulates to a complete toxic response and predict cellular pathways that a compound modulates to a complete support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information identifying the expression and for identifying toxicity markers in this changes in gene expression and for identifying toxicity markers in this database or cell apposed to a known toxicity markers in the proper in database or cell apposed to a known toxicity markers in the specification. The method is useful for elucidation and toxicity markers in the specification. state of tissue or cell tag (EST) or cDNA derived from a gene in response to a hepatotoxic agent. gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or sample that has been exposed to a compound or agent. Hepatotoxicity drug screening and toxicity assays. The genes and present characterised by centrilobular necrosis and steatosis. The sequence is an expressed sequence which is differentially expressed toxicity markers in

Sequence 292 BP; 67 A; 60 C; 86 G; 79 T; 0 other;

237 MetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluVal 256 278 GTGACACTGTCACAGGCAGAACCTGTTCCAAAGCACATTCCCACAGAAGCAGTCAAGGGT 219 257 TyraspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAla--- 275 276 ---AlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValVal 294 158 TACCCAAGTCTGTCCTTGGAAGAAATGCTCAAGAGATCTAATTCCATCGCTGCGGTCAGC 99 292 292 110 30 20 1 Length:
Matches:
Conservative:
Mismatches:
Indels: ValGlyLysLeuGlyThrSerThrValSerPro 305 98 GTCCAGGCCACAGGAACACAGTCCTCTTATCCA 66 Gaps: US-09-912-020-325 (1-477) x ABK63357 (1-292) ABL75687 standard; cDNA; 285 BP 0.102 112.00 54.93% 40.85% Best Local Similarity: Percent Similarity: Alignment Scores: ABL75687; Query Match: DB: Ŋ ABL75687 RESULT XXXX ò ద qq Ω g ö ă ò

-- LeuLysLeuAlaVal 332

328

316 AlaAspThrGlyPheGlyValMetThrGluGluGlu----

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(1-285)Gaps:

US-09-912-020-325 (1-477) x ABL75687

285 26 13 27 23

Conservative: Mismatches: Indels:

107.50 43.82% 29.21% 4.49%

Percent Similarity: Best Local Similarity:

Query Match:

0.257

Alignment Scores:

Matches: Length:

Sequence 285 BP; 65 A; 60 C; 74 G; 82 T; 4 other;

(or more) nucleic acid sequences.

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The present sequence describes a purified corn tassel-derived polynucleotide sequence (cdps) comprising a nucleic acid sequence polynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70637 to ABL70833. The cdps sequences encode corn tassel-derived polypeptides (CDPs). The cdps sequences (I) can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a transcript image.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel purified corn tassel-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vectors, to express a polypeptide, to identify, isolate or extend identical or related corn tassel nucleic acid sequences from DNA libraries, in nucleic acid hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two
                                                                              Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs; inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
                                        Corn tassel-derived polynucleotide (cdps) SEQ ID NO:5061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 5061; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sherman BK;
                                                                                                                                                                                                                                                                                                            99US-0294093
                                                                                                                                                                                                                                                                                                                                                  98US-082567P
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                SHERMAN B K.
                                                                                                                                                                                                                                                                                                                                                                                        LALGUDI R V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-163647/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    breeding programs
                                                                                                                                                                                                                           US2001051335-A1.
                                                                                                                                                                                                                                                                                                                                                  21-APR-1998;
14-MAY-2002
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The present invention describes a library of human polynucleotides comprising the sequences given in AAZ12532 to AAZ17779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell
                                                                                                                                                                                                                                                                                                                                                                58 ATCGTGAGCTTCGGCGAGATGCTCATTGAC-----TTCGTCCCGACCGTGTCGGGG 108
                                                                                                                                                                                                          ----GGGTTCCTCAAGGCCCCC 147
                                                                                                                                                                                                                                                                        ValMetValValGlyAspValMetLeuAspArgTyrTrpTyrGlyProThr---SerArg 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                      70 ValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeuAlaAspVal
                                                                                                                                                                   32 IleSer---ProGluAlaProValProValValLysValAsnThrIleGluGluArgPro
                                                                                                                                                                                                                                                    51 GlyGlyAla---AlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene expression product cDNA sequence SEQ ID NO:2105.
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Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA:
Jones WL, Kassam A, Kennedy GC, Kita D, Labat 1;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human genes and their expression products which are differentially expressed in different cell types
                                         US-09-912-020-325 (1-477) x AAA67292 (1-300)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 1136; 2479pp; English.
                                                                                                                                                                                           109 GTCTCCCTGCCGAGGCCCCG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 GGGGTCAACTGCGACGGCATCAAC 291
                                                                                                                                                                                                                                                                                                                                                                                                                       90 AsnValLysCysAspPheValSer 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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98US-0072910.
98US-0075954.
98US-0080114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ14636 standard; cDNA; 300
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  21
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(HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409938972-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-1999
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31-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences given in Expectation (E) value of 0.01 or less compared to the 835 sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic pathway in the plant. They are especially used to modulate or alter the polysaccharide content, composition or structure of the plant. ABB16268 to AABB16340 are proteins encoded by some of the polynucleotide sequence
                                                                                                                                                 Eucalyptus grandis; pinus radiata; Monterey pine; modification; plant cell wall; polysaccharide; polysaccharide biosynthetic pathway; transgenic plant; ds.
61 GTGAAAAGTCAGCTATCTCATANCCTTCCAACTTCTCGCCGGATCATGCAGTTTTCAAAT 120
                                         333 AlaAlaAlaArgLySArgGlyGluLySValValMetThrAsnGlyValPheAspIleLeu 352
                                                                               121 GGGCAGGCTCCTTCGCCAGGTGCTCGTGTTGTAGTAGATGGCACATTTGATCTTTC 180
                                                                                                                           HisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeuIleVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New genes encoding proteins involved in a plant polysaccharide blosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eucalyptus grandis D-fructokinase DNA sequence SEQ ID NO:293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
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17
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13
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                          373 AlaValAsnSerAspAlaSerThrLys 381
                                                                                                                                                                                                                                                  241 GTATCTATGGACGACGNATCGANTCAG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 150; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            given in the present invention.
                                                                                                                                                                                                                                                                                                                                      AAA67292 standard; DNA; 300 BP.
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99US-0148426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-NZ00169
                                                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2000 (first entry)
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84.50
51.14%
31.82%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eucalyptus grandis.
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Query Match:
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(ELIT-) ELITRA PHARM INC

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of the 5248 polynuclectide sequences given in AA212532 to AA217773. The polynuclectides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profilling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynuclectides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynuclectides may also be used to construct arrays for diagnostics (which may be used to determine function of an arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and lung cancer. The polynucleotides can also be used to screen for
       where the gene product is encoded by one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and lung cancer. The polynucleotide peptide analogues and antagonists.
suspected of being cancerous,
   $$$$$$$$$$$$$$$$$$$$$$$
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Sequence 300 BP; 70 A; 89 C; 92 G; 49 T; 0 other;

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188
                                                                                                                                                    200 GluAlaValValGlyLysCysLysThrGluGluGluIleValGluArgGlyMetLysLeu 219
                                                                                                                                                                                                                220 IleAlaAspTyrGluLeuSerAlaLeuLeuValThrArgSerGluGlnGlyMetSerLeu 239
                                                                                                                                                                                                                                      81 GTCGGAGGCCAGCAACTACCTGCACTT-----GCCGCCAGAGGGGCCAATCTTTT 131
                                                                                                                                                                                                                                                                         240 LeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspVal 259
                                                                                                                                                                                                                                                                                                                                   260 ThrGlyAlaGlyAspThrVallleGlyValLeuAlaAla-------ThrLeu 274
                                                                                                                                                                                                                                                                                                                                                               189 ACAGAGCAAAGTCCCTGGGCCCTGGGAAAAGCCTCATCACGGGCAGGGCTCTGGCCCCATA 248
                                                                                                                                                                                  21 GAGCAGACCCCAGGGCCTCTTAGCCAATCCCCGGGCCTGGTGAAGCAGGCGAAGCAGATG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli; identification; proliferation; microorganism; antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis; bacterial growth inhibition; ds.
                                                                                                                                                                                                                                                                                                     132 AGGTCTCTCGGGAAGGCCCCAGCCTCCCTCCCCACTGAAGAAGAAGAAGTTGGTA---ACC
                                                                                                                                                                                                                                                                                                                                                                                             275 AlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAla 289
                                                                                                                                                                                                                                                                                                                                                                                                               249 GTGGCTGGACAGACACTGGCACAGTCTTGCTGCTGCTGGGAGC 293
              300
21
23
42
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli nucleotide sequence SEQ ID NO:90.
               Length:
Matches:
Conservative:
                                                          Mismatches:
                                                                           Indels:
                                                                                                                       US-09-912-020-325 (1-477) x AAZ14636 (1-300)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH81291/c
ID AAH81291 standard; DNA; 245 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
               576
71.50
46.32%
22.11%
2.99%
                                                             Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                            Percent Similarity:
Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH81291;
                                                                           Query Match:
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               Pred.
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23-DEC-1999; 99US-0173005.

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The present invention describes a purified or isolated nucleic acid sequence (I) consisting essentially of one of the 93 nucleotide sequences given in AARB1202 to AARB1204, where expression of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism.

(I) have antibacterial and antibiotic activities, and can be used in gene therapy. Expression of (I) in a microorganism inhibits proliferation of the microorganism, and the manufactured antibiotic is useful for reducing the activity or level of a gene product required for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used as antisense therapeutics for killing bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as antisense that are specific for particular species of microorganisms can be used as probes to identify particular species of microorganisms can be used as probes to identify particular microcranism species in clinical specimens. AAHB1295 to AAHB1487 encode the Escherichia coli proteins given in AAG98239 which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corn; corn tassel-derived polynucleotide; cdps; hybrid breeding; CDPs; inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene; ss.
                                                                                                       Novel nucleic acids encoding proteins required for Escherichia coli
proliferation, useful for screening for antimicrobial agents -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corn tassel-derived polynucleotide (cdps) SEQ ID NO:3810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 G; 80 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
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                                   Zyskind JW;
                                                                                                                                                           Claim 1; Page 129; 596pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL74436 standard; cDNA; 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 A; 53 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-082567P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.00
100.00%
100.00%
2.93%
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                                   Ohlsen KL,
                                                                    WPI; 2001-457376/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 245 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
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                                 Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-DEC-2001
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Mycobacterium tuberculosis; Mycobacterium bovis; mycobacterium;
             Eucalyptus grandis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XX DX DX XX
                                                                                                                                                                                                          polynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL76833. The cdps sequences encode corn tassel-derived polypeptides (CDP9). The cdps sequences (I) can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a transformation vectors, to express a polypeptide, to identify, isolate or extend identical or related corn tassel nucleic acid sequences from DNA isolates or used in nucleic acid hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two
                                                                                                      Novel purified corn tassel-derived polynucleotide useful for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 AspThrGlyPheGlyValMetThrGlu-------GluGluLeuLySLeuAla 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 ValAlaAlaAlaArgLysArgGly------GluLysValValMetThrAsnGly 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bucalyptus grandis; pinus radiata; Monterey pine; modification;
plant cell wall; polysaccharide; polysaccharide biosynthetic pathway;
transgenic plant; ds.
                                                                                                                                                                                                  The present sequence describes a purified corn tassel-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eucalyptus grandis D-fructokinase DNA sequence SEQ ID NO:279.
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18
6
20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 287 BP; 78 A; 57 C; 69 G; 83 T; 0 other;
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
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                                                                                                                                                                       Claim 1; SEQ ID 3810; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (or more) nucleic acid sequences.
                                                    Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
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67.50
45.28%
33.96%
2.82%
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                                                    Ito LY,
                       SHERMAN B K.
LALGUDI R V.
                                                                             WPI; 2002-163647/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                              breeding programs
                                                    RV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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           (ITOL/)
(SHER/)
                                                    Lalgudi
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g
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The present invention describes isolated polynucleotides (PN) comprising a sequence selected from one of 835 nucleotide sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences given in AAA67073 to AAA67907, their (reverse) complements, sequences producing an Expectation (E) value of 0.01 or less compared to the 835 sequences at least 50% identical to them, 200, 100, 40 or 20-mers of the 835 sequences that are degenerately equivalent or allelic to the 835 sequences. The polynucleotides are used to modify the activity of a polypeptide involved in a polysaccharide biosynthetic polysaccharide content, composition or structure of the plant. AAB16268 to AAB16340 are proteins encoded by some of the polynucleotide sequence given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 ThrGlyAlaGlyAspThrVallleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSer 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 ATTCTCGAAGATGAAGAAAATTGAGGAAAGTCCTGAAGTTTGCAAACGCGTGCGGAGCC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genes encoding proteins involved in a plant polysaccharide biosynthetic pathway, useful for modulating or altering the polysaccharide content, composition or structure of the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 ValValValGlyLysLeuGlyThrSerThrValSerProIleGluLeuGlu 309
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17
5
7
7
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                    (FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                          (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 146; 301pp; English.
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                                                                                                       99WO-NZ00169
                                                                                                                                                            98US-0170862
99US-0148426
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40.35%
29.82%
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WO200022092-A2
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                                                                                                                                                                                                                                                                                                                      3loksberg LN;
                                                                                                                                                            13-OCT-1998:
                                                                                                       08-OCT-1999;
                                                                                                                                                                                        11-AUG-1999;
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                                                     20-APR-2000.
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                                                                                                                                                                                                                                                                                                   The present invention describes a method for isolating a polynucleotide of interest that is present or is expressed in a genome of a first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain, which is different from the first strain using a bacterial artificial chromosome (BAC) vector. Recombinant BAC vectors, which are preferably immobilised, can be used to detect mycobacterial nucleic acids (genomic DNA, cDNA or mRNA) in biological samples. The polynucleotides identified are useful as probes or primers for detecting a given mycobacterium of interest. By aligning the polynucleotides contained in the recombinant BAC vectors it is possible to physically map a polynucleotide of mycobacterial origin in a re useful in providing information for combating tuberculosis. It is possible to compare genomes between different strains or species and their non-pathogenic strains or species conterparts. ABG62492 to ABG63228 and ABB81227 to ABB81220 represent sequences used in the compare contentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 AsnAlaValArgGlyArgAlaAspThrGlyPheGlyValMetThrGluGluGluLeuLys 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367
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detection; BAC vector; bacterial artificial chromosome; tuberculosis;
gene; ds.
                                                                                                                                                                                                                                          useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 AATCTGGCGCCTGGCCGACCACGTGCGCGTAGGCTTG-----CGATCGTGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161 GCTGGCGTGGCCAGGACGAGATCCCGACGATTGGGGC-AGATGCGTGCTCACCATCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValPheAspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 LeuAlaValAlaAlaAlaAlaArgLysArg-----GlyGluLysValValMetThrAsnGly
                                                                                                                                                                                                                                         Isolation of polynucleotides from mycobacterial genomes, detection of Mycobacteria and for combating tuberculosis
                                                                                                                                                                                        Billault A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279
222
6
727
6
729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 279 BP; 37 A; 94 C; 105 G; 43 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                           Gordon S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-912-020-325 (1-477) x ABQ63223 (1-279)
                                                                                                                                                                                                                                                                               Claim 27; Page 127; 161pp; English.
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                                                                                                                                                                                           Buchrieser-Brosch R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.88e+03
65.50
46.67%
36.67%
2.74%
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                                                                                                                 99WO-IB00740.
                                                                                                                                       98US-0060756
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                                                                                                                                                                  (INSP ) INST PASTEUR
                                                                                                                                                                                                                 WPI; 2000-013262/01.
                                      bovis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                      Mycobacterium
                                                             W09954487-A2
                                                                                                               16-APR-1999;
                                                                                                                                        16-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                      8-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH52260;
                                                                                                                                                                                           Cole S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348
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AAH52093 to AAH52303 encode the human secreted proteins given in AAG81242 to AAG81453. The secreted proteins can be used for directing the secretion of proteins of interest from a host cell including bacteria, fungal cells, and cultured higher entaryotic cells. The present invention also describes fusion proteins, where a secreted protein of the invention protein selected from the group consisting of maltose binding protein, an immunoglobulin constant region, a polyhistidine tag and a peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 ProGlnProLeuHisGluArgIleAsnGlnAlaLeuSerSerIleGlyAlaLeuValLeu 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 SerAspTyrAlaLysGlyAlaLeuAlaSerValGlnGlnMetIleGlnLeuAlaArgLys 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 AlaGly------ValProValLeuIleAspProLysGlyThrAspPheGluArgTyr 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 GTTGGGAAAGTTGTGTTCCCGAGACTACAGGATAAAAAATACTATGAT---AAGAAATAC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated polypeptide for directing secretion of proteins of interest from a host cell including, e.g. bacteria, includes contiguous amino acid residues of polypeptide with specified amino acids \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 GGTGCCTGTGCCTCAGGGGATTTCGCTTCTGTACAGGAAGCAATGGCCAAAAATGAGCAAA
                                                     cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187 ArgGlyAlaThrLeuLeuThrProAsnLeuSerGluPheGluAlaValVal 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 CAAGTATTCCTGAAGCTGGTTGAACACCCAGAAGGAGTATTTGGCGATCATG 225
                                            Human; secreted protein; secretion; bacterial cell; fungal eukaryotic cell; fusion protein; maltose binding protein; immunoglobulin constant region; polyhistidine tag; ss.
Human AFP protein encoding cDNA sequence SEQ ID NO:335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237
24
12
35
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 556; 617pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-912-020-325 (1-477) x AAH52260
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                                                                                                                                                                                                                                                                                                                                                                                                   990S-0160712
                                                                                                                                                                                                                                                                                                                                           20-OCT-2000; 2000WO-US29052
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46.75%
31.17%
2.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZYMO) ZYMOGENETICS INC
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Best Local Similarity:
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                                                                                                                                                                                                                           WO200129221-A2.
                                                                                                                                                                                                                                                                                                                                                                                                20-0CT-1999;
                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conklin DC,
                                                                                                                                                                                                                                                                                   26-APR-2001
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ABL38371
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BP.

(first entry)

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US-09-912-020-325 (1-477) x ABL76194 (1-298)
                           ABL76194 standard; cDNA; 298
                                                                                        14-MAY-2002
                                                         ABL76194;
            ABL76194/c
RESULT 14
                                           ABL36412 to ABL38645 represent human colon tumour antigen cDNA clones (I) which were isolated from human colon tumour and colon metastatic tumour cDNA libraries. (I) have cytostatic activity and can be used in vaccine production. (I) can be used for stimulating and/or expanding T cells specific for a tumour protein on contact with the T cells. They are also useful for inhibiting the development of cancer in a patient. (I) can be used as probes or primers for nucleic acid hybridisation, for preparing mutant species primers, or primers for use in genetic constructions. (I) can be used in the diagnosis of a colon tumour.
                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated colon tumor polynucleotide differentially expressed in colon tumor or colon metastatic tumor and polypeptides encoded by them, useful for inhibiting development of cancer in patient -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 AlaGlyvalValValGlyLysLeuGlyThrSerThrValSerProIleGluLeuGluAsn 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 AlaValArgGlyArgAlaAspThrGlyPheGlyValMetThrGluGluGluLeuLysLeu 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------IleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGly 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 AlaValAlaAlaAlaArgLySArgGlyGluLySValValMetThrAsnGlyValPheAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 ATGGAATCCATGGTCCATGCAGACACAAGATCATTTATTCTGAAGAAGCCAAAGCTGTCT
                                                                        colon cancer; colon tumour antigen; cytostatic; vaccine; tumour metastatic antigen; diagnosis; gene; ss.
                                         Human colon tumour antigen polynucleotide SEQ ID NO:1960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGGAAGTAGTGGCACCAAACCAAGAGTCGGGGATGAAG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspArgLeuIleValAlaValAsnSerAspAlaSerThrLys 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G; 54 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-912-020-325 (1-477) x ABL38371 (1-275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 1960; 105pp; English.
                                                                                                                                                                                                                                                                                                                          Secrist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 97 A; 58 C;
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64.00
39.36%
24.47%
2.67%
                                                                                                                                                                                                                                           09-JUN-2000; 2000US-210899P.
20-FEB-2001; 2001US-270216P.
                                                                                                                                                                                                                08-JUN-2001; 2001WO-US18557
           (first entry)
                                                                                                                                                                                                                                                                                                                        Jiang Y, Harlocker SL,
                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-114514/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                   WO200196388-A2
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                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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                                                                                         colon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
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polynucleotide sequence (cdps) comprising a nucleic acid sequence selected from those given in ABL70627 to ABL7683. The cdps sequences encode corn tassel-derived polypeptides (CDPs). The cdps sequences (concode corn tassel-derived polypeptides (CDPs). The cdps sequences (I) can be used for determining altered gene expression, to recover regulatory elements and to follow inheritance of desirable characteristics through hybrid breeding programs. (I) are also useful in the evaluation, and alteration of desirable. (I) are also useful in the evaluation, and alteration of desirabce, environmental adaptability, quality and yield, and as molecular markers for studying inheritance of multigene traits in a plant breeding program. (I) can be used to produce a tassel-specific profile of gene transcription, a transcription, a colone regulatory elements for used it transformation vectors, to express a polypeptide, to identify, isolate or extend the produce or transcription is the colone regulatory elements for used in transformation vectors, to express a polypeptide, to identify, isolate or extend the produce of the colone regulatory elements for produce is the colone regulatory elements for used in transformation vectors, to express a polypeptide, to identify, isolate or extend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ermining altered gene expression, to recover regulatory elements and follow inheritance of desirable characteristics through hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             libraries, in nucleic acid hybridisation or amplification technologies, as query sequences to determine homology of known sequences, as probe for use in Southern or Northern hybridisation, and to identify the presence of and/or to determine the degree of similarity between two
                                                                          cdps; hybrid breeding; CDPs;
                                                                                                         inheritance; characteristic; growth; development; disease resistance; environmental adaptability; quality; yield; molecular marker; multigene trait; plant breeding; corn tassel; gene: ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence describes a purified corn tassel-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     purified corn tassel-derived polynucleotide useful for
Corn tassel-derived polynucleotide (cdps) SEQ ID NO:5568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298
25
14
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18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
                                                                          Corn; corn tassel-derived polynucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 5568; 201pp; English:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sherman BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.81e+03
64.00
37.50%
24.04%
2.67%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (LALG/) LALGUDI R V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SHER/) SHERMAN B K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-163647/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determining altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              breeding programs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                       JS2001051335-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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55 G; 64 T; 0 other;

66 A; 82 C;

Sequence 267 BP;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human brains \boldsymbol{\cdot}
                                                                                                                                        177 GGGCTCAGAAGCCAGGGGTTGGTGGCGCCAATGATCTTGCGGCCAGTTGTGACGACGCT 118
                           297 CCAATCAGCAGGGCCCTCGGGGAACCNCAGGGCAATCTCCTTATTAGCACTCTCAATGCT 238
                                                                       LeuAlaAspValAsnValLysCysAspPheValSerValProThrHisProThrIleThr 105
                                                                                                                                                                                                                               106 LysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAspPheGluGluGlyPhe 125
                                                                                                              82
                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                            ----CACAGGGCCAGAGATGATGTAGTCCACGAGGCCCTGGAAGAGGGCTT 46
ProThrSerArgIle ---- SerProGluAlaProValProValValLysValAsnThr 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
epilepsy; cancer; ss.
                                                                                                                66 AsnAlaArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSer
                                                      46 IleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAla
                                                                                                                                                                                                  Example 4; SEQ ID NO: 17801; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human brain expressed single exon probe SEQ ID NO: 17801
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ID AAK17810 standard; DNA; 267 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-2000; 2000US-0234687
27-SEP-2000; 2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                         126 GluGlyValAsp 129
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                                                                                                                                                                                                                                                                                                                   45 GGAGGCGCAGAT 34
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                                                                                                                                   23 ArgTyrTrpTyrGlyProThrSerArgIleSerProGluAlaProValProValUys 42
                                                                                                                                                                                        43 ValAsnThrIleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSer
                                                                                                                                                                                                                                                                       152 TTGGGAGTGAGCTCTTGTGAGTCACAGGTTGGGGCTTCCCTGTGTAACCTGGTGAGGCTC
                                                                                                                                                                                                                                                                                                    73 ThrGlyIleAsp-----AspAlaAlaArgAlaLeuSerLysSerLeuAlaAspVal
            267
23
13
28
17
                                      Conservative:
Mismatches:
Indels:
            Length:
Matches:
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          2.71e+03
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44.44%
28.40%
2.65%
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                                      Percent Similarity:
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9
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MODEL-frame+_p2n.model -DEV-xlp
-Q=CQGn2_1/CAPPO_spool/USQ91220_Vunat_20112002_150300_111098/app_query.fasta_1.647
-Q=CQGn2_1/CAPPO_spool/USQ991202_Dns21n300.rst -MINATCH=0.1 -LOOPECL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=-CT -THR_MAX=100 -AIRGN=15 -MODE=LOCAL
-OUTFMT=btc -NORM=axt -HBAPSIZE=500 -MINLEN-0 -AAXLEN=300
-USER=USO9912020_CGGN_11_2024_Grunat_20112002_150300_11098 -NCPU=6 -ICPU=3
-NO_XLRX - NO_MANP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGIGG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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1 MKVTLPEFERAGVMVVGDVM......FEDGCSTTNIIKKIQQDKKG 477
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                          Compugen Ltd
                                                                                            OM protein - nucleic search, using frame_plus_p2n model
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compuq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16154066 seqs, 8097743376 residues
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Maximum Match 100%
Listing first 45 summaries
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em_gss_other:* em_gss_pro:*

em_gss_rod:*

em_gss_pln:* em_gss_fun:* em_gss_mam:* em_gss_mus:*

em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	20	AI236089 AI23608	AU072448 AU07244	1877/9/ H32/9/	AU100188 AU10018	4 BM903102 BM9031	2 BF755713 BF7557	0 BB130904 BB1309 0 AW565187 AW5651	0 AW782015 AW7820	4 BQ634379 BQ6343	4 BQ097023 BQ0970 AA113615 AA11361	4 BQ041062 BQ0410	3 BI200260 BI2002	3 BMID8266 BMID82	0 BB355746 BB3557	4 W17420 W17420	4 BQ635002 BQ6350 2 BE659338 BE6593	0 AV413900 AV4139	2 BG157882 BG1578	4 C55835 C55835	4 C5/1/5 2 BF226625 BF2266	AV083373 AV08337	024	AA432985 AI974677 AI974677	AI616187 AI616187 vr66d04.	2 BF849567 BF849567 IL5-ENC	3 BI423558 BI42355	2 BE854380 ux29f02	AA356818 AA356818	A1426060 A1426060	2 BF585739 FM1_24	3 BM418225 BM418225 952004F	A1103200 A0562483 A0552483 AV55248	4 BQ046251 BQ04629	ALIGNMENTS			263 bp mRNA linear EST 21-MAR-20 er cDNA library (OLe) from HNI Oryzias latipes	a similar e (EC 2.7.	ces pombe), mRNA sequence.	428129		a; Chordata; Craniata; Vertebrata; Euteleostomi;
	Length D	263 182	292	240	0.40	300	235	242	150	297	249	260	289	256	241	270	236	288	295	224	300	247	246	251	700 700 700	110	243	279	292	226	298	218	218	256	258				edaka	OLe06. ransfer	λmc	GI:13	medaka.	dulpes ; Metazoa;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 182)
Marray, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 IleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeu 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 ATAGTGGGCGTGCACACAGATGAGGAGTTTCCAAACACAAGGGCCCC-----CCCGTC 180
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                                                                                                                                                                                                                                                                                                                                /clone_lib="Medaka liver cDNA library (OLe) from HNI"
/tissue_type="liver"
/dev_stage="adult"
75 c 89 g 37 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                331 AlavalAlaAlaAlaArgLysArgGlyGluLysValValMetThrAsnGlyValPheAsp 350
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                                                                                 Contact: Kiyoshi Naruse
Department of Biological Sciences
Graduate School of Science, University of Tokyo
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Tel: 81-3-5841-4443
Fax: 81-3-5841-4410
Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from Medaka liver cDNA library (OLe).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Beloniformes; Adrianichthyidae; Oryzinae; Oryzias
                1 (bases 1 to 263)
Naruse,K., Mitani,H. and Tanaka,M.
Medaka EST Project in University of Tokyo (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          263
129
30
12
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Conservative:
Mismatches:
Indels:

    .263
    /organism="Oryzias latipes"

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Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                  /db_xref="taxon:8090"
                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                /clone="OLe06.08a"
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/USGILEM. MUS.CHILO.
/USGILEM. MUS.CHILO.
/UD.XTEF="Laxon:10090"
/Clone="INDAGE:1125607"
/Clone=Lib="Knowles Solter mouse 2 cell"
/Lissue_type="embryo"
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/note="Organ: embryo; Vector: pBluescribe (modified);
/lab_host="DH10B"
/note="Organ: embryo; Vector: pBluescribe (modified);
/lab_host="DH10B"
/la
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EST232651 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone ROVIDS293' end, mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Washington University School of MedicineP 4444 Forest Park ParkWay, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@Watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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Rat Genome Project: Generation of a Rat EST (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 IleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArgLeu
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The Institute for Genomic Research
9712, Medical Center Drive, Rockville,
Tel: (301)-838-3529
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:44689"
/clone="SSE551"
/clone_lib="Dictyostellum discoldeum SS (H.Urushihara)"
                                                            MetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluVal 256
                                                                                                                                                                                                                                                                                                                                        GIGACACTGTCACAGGCAGAACCTGTTCCAAAGCACATTCCCACAGAAGCAGTCAAGGCT 219
                                                                                                                                                                                                                                                                                                                                                                             257 TyrAspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAla--- 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                158 TACCCAAGTCTGTCCTTGGAAGAAATGCTCAAGAGATCTAATTCCATCGTGCGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: hidekoébiol.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA project in Japan.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Developmental cDNA in Dictyostellum discoideum (1999) Unpublished (1999) Contact: Hideko Urushihara Institute of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Mycetozoa: Dictyosteliida: Dictyostelium
1 (bases 1 to 240)
Urushihara,H.
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1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572,
Tel: 81-298-53-4664
Fax: 81-298-53-6614
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Matches:
Conservative:
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AU072448.1 GI:5162637
EST.
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             Email: nhiee@tigr.org
Seg primer: M13-21.
Fax: (301)-838-0208
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112.00
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432797 22-APR-1998 EST108244 Rat PC-12 cells, untreated Rattus sp. cDNA clone RPCCJ755 end similar to Cholinephosphate cytidylyltransferase, mRNA
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Lee, N.H., Weinstock, K.G., Kirkness, E.F., Earle-Hughes, J.A., Fuldner, R.A., Marmaras, S., Glodek, A., Gocayne, J.D., Adams, M.D., Kerlavage, A.R., Fraser, C.M. and Venter, J.G. comparative expressed sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth
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/clone_lib="Rat PC-12 cells, untreated"
/note="Vector: paluescript SK:, Site_1: EcoRI; Site_2:
XhoI; poly(A)+ RNA was purified from untreated PC12 cells cultured for 9 days. CDNA was constructed using an oligo-dT primer and directionally cloned using the Lambda
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                            343 ValMetThrasnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsn 362
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The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD
9712, Medical Center Drive, Rockville, MD
Fax: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
For clone availability please contact th
(tdbinfo@tdb.tigr.org)
Seq primer: M13 Reverse
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/db_xref="ATCC (inhost):2002922"
/db_xref="taxon:10118"
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us-09-912-020-325.p2nszlm300.rst

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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Dictyostelium discoideum"
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/db_xref="taxon:44689"
/clone="SSK263"
/clone="Ib="Dictyostelium discoideum SS (H.Urushihara)"
/dev_stage="slug"
/dev_stage="slug"
/dev_stage="slug"
                                                                                                                                                                                                                                                                         343 ValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsn 362
                                                                                                                                                                                                359 TyrLeuAlaAsnAlaArgLysLeuGlyAspArg-----LeuIleValAlaValAsnSer 376
                                                                                                                                                                                                                  339 GlyGluLysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSer 358
                                                                                                                                                                                                                                                       377 AspAlaSerThrLysArgLeuLysGlyAspSerArgProValAsnProLeuGluGlnArg 396
                                                                                                                                                                      9
                                                                                                                                                          Japan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Developmental cDNA in Dictyostellum discoideum (1999)
Unpublished (1999)
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 240)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan Tel: 81-288-53-4664 Eax: 81-298-53-6614 Eax: 81-298-53-6614 Eax: 81-298-53-6614 Eax: 81-298-53-6614 Eax: 81-298-53-6614 Eax: 81-28-62110m discoideum cDNA project in PROJECT - Dictyostellum discoideum cDNA project in Location/Qualifiers
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AU074294.1 GI:5180715
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (bases 1 to 300)

Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo, K., Suyama,A. and Sugano,S.

In silico mapping of the 5'-ends of human mRAs using full-length enriched and 5'-end enriched cDNA libraries constructed by Oligo-capping method enriched cDNA libraries constructed by Unpublished (2001)

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-hakagawa,K., Maruyama,K., Suyama,A. and Sugano
s.S. Construction and characterization of a full length-enriched and
a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AU100188 Sugano Homo sapiens CDNA library Homo sapiens cDNA clone REC00707 similar to Homo sapiens mRNA for phosphoethanolamine cytidylyltransferase, mRNA sequence.
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/do_xef="teaxon:5606"
/clone="RECO0707"
/clone=lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and dimethylfumarate treated U937 cells"
3 90 c 117 g 40 t
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-----AspThrGlyPheGlyValMetThrGlu 325
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                                                                                                                                                                                                                                        163 AATAAAGGTCCA-----CCAGTTATGAATGAACAAGAAAGA------TATAAAGCA 207
                                                                           363 AlaArgLysLeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThrLysArg
                                                                                                                             26 ecrercecececececerecesescentearecesaaceseceseseseseseses
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PM4-CT0562-291000-002-910 CT0562 Homo sapiens cDNA, mRNA sequence.
BF755713
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Rels, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed
  324 ThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysValVal 343
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20202663
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clone NXLV_079_E07 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
                                            133 GATGGCTGCTATGACATGGTGCATTACGGCCACTCCAACCAGCTGCGCCAGGCACGGGCC 192
                                                                                           366 LeuGlyAspArgLeuIleValAlaValAsnSerAspAlaSerThrLysArgLeuLysGly 385
                                                                                                                    236 GlyMetSerLeuLeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGlu 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular Basis of Wood Formation in the Pine Megagenome Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                                                   CCC-----CCGGTGTTCACTCAGGAGGAGATACAAGATGGTGCAGGCCATC 300
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    .235
    /organism="Pinus taeda"

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Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T. T. Z. Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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URL.http://genome.gsc.riken.go.jp,
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                                                                                                                                                                                                                                                                                                                                                                                                                          EST 29-JUN-2000
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 202)
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344 MetThrAsnGlyValPheAspIleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAla 363
                                     364 ArgLysLeuGlyAspArg-----LeuIleValAlaValAsnSerAspAlaSerThrLys 381
                                                                                                                                                                        103 CACAGGCTGGCAGAGGCCCTACATCATCGCGGGCTTACACTTTGACCAGGAGGTCAAT 44
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/clone_lib="RIKEN full-length enriched, 16
                                                                                                                                                                                                                                         382 ArgLeuLysGlyAspSerArgProValAsnProLeuGlu 394
                                                                                                                                                                                                                                                                                                    43 CACAACAAGGGGAAGAACTACCCCATCATGAATCTGCAA 5
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/dev_stage="16 days neonate"
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AW565187 19-JUL-2000 LG1_328_B07.b1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
/note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was primed with a primer [6].
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sorghum bicolor
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoideae, Andropogoneae, Sorghum.
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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Contact: Cordonnier-Pratt MM
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loblolly pine.
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Best Local Similarity:
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Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,M., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: cou@resgen.com
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297 bp mRNA linear EST 03-DEC-2001

S199602.1 Gm-c1027 Glycine max CDNA clone GRNOME SYSTEMS CLONE ID:
Gm-c1027-7539 5' similar to TR:Q9VV19 Q9ZV19 PUTATIVE
PHOSPHOETHANOLAMINE CYILDYLYLTRANSFERASE. ; mRNA sequence.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                          1. 150
/drganism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Light Grown 1 (LG1)"
/note="Yorgan: 10- to 14-day-old light-grown (greenhouse)
/note-Torgan: 10- to 14-day-old light-grown (greenhouse)
/note-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torganism-Torg
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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Seq primer: JEN REV
High quality sequence stop: 25
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                                                                                                             Location/Qualifiers
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Fax: 314 286 1810
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/note="Vector: pBluescript II SK+; Site_I: ECORI; Site_2:
Xhoi; This CDNA library was constructed from mRNA isolated
from cotyledons of 3- and 7-day-old williams seedlings
which were propagated on paper towels with distilled
water. The cotyledons were flash-frozen in liquid
nitrogen, then lyophilized for 72 hours. Unequal amounts
of mRNA was used for cDNA synthesis. Stratagene's cDNA
Synthexix Kit (catalog number 200401) was used to
synthexix Kit (catalog number 200401) was used to
synthexiz the cDNA. First- stranded synthesis was
performed with 5-methyl dcTP, hone the ligated cDNA was
hemimethylated. A modification of Stratagene's
first-strand synthesis primer was used. An anchor
nucleotide (V-A, C, or G) was added to the 3' end of the
primer [GAGAGAGAGAGAGAGAAACATAGTTCTCAG(T)18] to anchor
the primer at the 5' end of the poly(A) tract. After
second strand synthesis, the cDNA ends were filled in
with cloned Pfu DNA, ligated to ECORI adapters and
subsequently phosphorylated. The XhoI site within the
first-strand synthesis, piner was then restricted by
digestion with XhoI; all XhoI sites in the cDNA
constructs were size-fractionated with a 500 bp cutoff,
using GibcoBRL Life Technologies' CDNA Size Fractionation
Stratagene's spluescript(m) II XR Fredigested vector
(pBluescript II SK(+) that has been digested with ECORI
and XhoI, and phosphorylated by Stratagene). 97% of the
white and blue colonies appear to content necombinant
plasmids with cDNA inserts, based on size (n=30). This
library was constructed by DI. Paul Keim and DI. Virginia
COVPAIL."
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                                                                                                                                                                                                                                                             /tissue_type="cotyledons of 3- and 7-day-old Williams seedlings"
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                                                                                                                                                                                                          /clone="GENOME SYSTEMS CLONE ID: Gm-c1027-7539"
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                                                                                                                                     /organism="Glycine max"
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                                                                                                                                                                                                                          /strain-"Coastal plain loblolly pine from North Carolina" /db_xref-"taxon:3352"
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 249)
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                                                                                                                                                                                                                                                            /clone="NXRV068_C02"
/clone_lib="NXRV (Nsf Xylem Root wood Vertical)"
/tissue_type="Xylem"
                                                           Molecular Basis of Wood Formation in the Pine Megagenome
                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 others
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                                                                                                                                                                                                                                                                                                       /cell_type="Root (primary)"
/dev_stage="Transitional"
/lab_host="XL1-Blue"
                                                                                                                                                                                                  1. .249
/organism="Pinus taeda"
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                                                                         Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
                                                                                                                    Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 CTGACGGAA---AACATTGCGATCGAC 246
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                                             Sederoff, R.
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Coniferopsida, Coniferales, Pinaceae, Pinus, Pinus. 1 (bases 1 to 268)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 bp mRNA linear EST 08-NOV 0662R Pyrococcus furiosus 1-2AP II library, F Robb Pyrococcus furiosus cDNA similar to TRANSFERASE, GLYCEROL-3-PHOSPHATE CYIDDILY, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 AlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArgLeuValGlyLeuThrGlyIleAsp 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 ValProValValLysValAsnThrIleGluGluArgProGlyGlyAla---AlaAsnVal
                                                                        Molecular Basis of Wood Formation in the Pine Megagenome
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Conservative:
Mismatches:
Indels:
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                                                                                       Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                                                            1. .268
/organism="Pinus taeda"
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1 (bases 1 to 260)
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AA113615.1 GI:1665570
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Pyrococcus furiosus
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                                                      Sederoff, R.
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Robb, F.T.

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Search completed: November 25, 2002, 00:59:48 Job time: 2371 secs

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190, App 2418, Ap 1, Appli

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Sequence:

Title:

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Sequence 97, Appl Sequence 9, Appl1 Sequence 5, Appl1 Sequence 290, App Sequence 265, App
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Sequence 186, Application US/08651155B
Patent NO. 6365401
GENERAL INFORMATION:
APPLICANT: Mainan Dr., Michael J.
APPLICANT: Mainan Dr., Christopher P.
APPLICANT: Hiethoff Mr., Douglas M.
TITLE OF INVENTION: METHOD AND PROBES FOR THE IDENTIFICATION
TITLE OF INVENTION: INFECTION
NUMBER OF SEQUENCES: 255
CORRESPONDENCE ADDRESS:
                                                                           Sequence 1
Sequence 1
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Sequence 8
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PCT-US95-05980-97
                                                                                                                                                                                                                                                                                                                                                                 US-08-673-190A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/651,155B
FILING DATE: 17-MAY-1996
CLASSIFICATION: 514
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Petersen Mr., Steven C.
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 17060.1
TELEPHONE: 303/546-1300
TELEFAX: 303/449-5426
  TELEX: ABA1475
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-0=-fssued_Patents_1M -QFWT=fastap -SUFFIX-priszln300.rnl -MINAATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62
-TRANS=human40.cdl -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT—pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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                                                                                November 24, 2002, 23:20:29; Search time 74 Seconds (without alignments) 1976.822 Million cell updates/sec
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
             GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                              nucleic search, using frame_plus_p2n model
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US-09-060-756-722
US-08-716-942-22
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US-08-105-168B-4
US-08-698-948-4
US-09-060-756-209
US-08-818-111-37
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Maximum Match 100%
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Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alain
TITLE OF INVENTION: HEADON FOR ISOLATING A POLYNUCLECTIDE OF INTEREST FROM
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060;756
CURRENT FILING DATE: 1998-04-16
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: OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GAGCTGGAAAACGCAGTGCGCGGACG----GATACCGGCTTCGGCGTTATGACCGAAGAG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 AlaAsnAlaAlaAlaGlyValValValGlyLysLeuGlyThrSerThrValSerProIle 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPheGlyValMetThrGluGlu 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 GluLeuLysLeuAlaValAlaAlaAlaArgLysArgGlyGluLysValValMetThrAsn 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 ---GCGTTCGATATCTGACGCCATTATGACGCAACTGGACCTATCGGATACTTA 281
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Mismatches:
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APPLICANT: Cole, Stewart
 186:
                              LENGTH: 294 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Mycobacterium bovis
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263.00
79.59%
73.47%
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 722
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65.50
36.15%
27.69%
INFORMATION FOR SEQ ID NO:
                  SEQUENCE CHARACTERISTICS
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APPLICANT: Terragen Diversity Inc.
APPLICANT: Radomski, Christopher C. A.
APPLICANT: Seow, Kah Tong
APPLICANT: Warren, R. Antony J.
APPLICANT: Yap, Wai Ho
TITLE OF INVENTION: METHOD FOR ISOLATING XYLANASE GENE
TITLE OF INVENTION: SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD
TITLE OF INVENTION: COMPOSITIONS OBTAINED THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGlnProGlyLysAlaProLeuHisMetProThrGlnAlaGlnGluValTyrAspVal 259
                                                                                                                                                                                                                                                                    280 LeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLySLeuGly 299
                                                                                                                                                                                                                                                                                                                                                                                              101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 PheGlyValMetThrGluGluGluLeuLysLeuAlaValAlaAlaAlaArgLysArg--- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 GTAGGCTTG------CGATCGTGCAGCGCTGGCGTGGCCAGGACGAGATCCCGACGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- GlyGluLysValValMetThrAsnGlyValPheAspIleLeuHisAlaGlyHisVal 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 ATTGGGGC-AGATGCGTGCTCACCATCGGGGTATTTGACGGCGCGCCCCGCGGGCACGCC
                                                                                                                                                               300 ThrSerThrValSerProlleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGly
                                                                                                                                                                                                                                   260 ThrGlyAlaGlyAspThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSer
  40
                                                                           US-09-912-020-325 (1-477) x US-09-060-756-722 (1-280)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Oppedahl & Larson
STREET: 1992 Commerce Street, Suite 309
CITY: Yorktown Heights
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 SerTyrLeuAlaAsnAlaArgLysLeuGly 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 GAACTGATCGCGCACGCGGTCAAAGGCGGC 280
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/004,157
FILLING DATE: 20-Sep-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/08716942
Patent No. 5849491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32,038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (914) 245-3252
TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Marina T. Larson
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Word Perfect
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  2.748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM COMPOPERATING SYSTEM:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MABILAT et al
TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE
TITLE OF INVENTION: MYCOBACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                              204 GTGGCTCCAGAGGCTGTCCCGCCACGCGCGCCGTCGTCGGTCACCTGCTCGTTGACGAC 145
                                                                                                                                                                                                                                                                                                                              32 IleSerPrcGluAlaProValPro-----ValValLysValAsnThrIleGluGlu 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 GlyValMetValValGlyAspValMetLeuAspArgTyrTrpTyrGlyProThrSerArg 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 ArgLeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeuAla
; OTHER INFORMATION: Description of unknown organism: soil microbe US-09-130-337A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 AspvalAsnvalLysCysAspPhevalServalProThrHis 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------CGACGCCGGCTTCTGCGCGTACCACCAC 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: J11ff & Berridge
STREET: 700 South Washington Street, Suite 300
CITY: Alexandria,
STATE: Virginia
ZIP: 23314
                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                         US-09-912-020-325 (1-477) x US-09-130-337A-22 (1-294)
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Matches:
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CURRENT APPLICATION DATA:
FILING DATE: ANGUST 12, 1993
APPLICATION NUMBER: US/08/105,168B
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
FILING DATE: August 8, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: WPB 28835 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: William P. Berridge
REGISTRATION NUMBER: 30,02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-2787
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: 31iff & Bastreet: 700 South War
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                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                    Alignment Scores:
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APPLICANT: Warren, RAJ
APPLICANT: Warren, RAJ
APPLICANT: Warren, RAJ
TITLE OF INVENTION: METHOD FOR AMPLIFICATION OF XYLANASE GENE FRACMENTS
TITLE OF INVENTION: FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AND COMPOSITIOT TITLE OF INVENTION: THEREBY
FILE REFERENCE: 9993-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264 GGGGTCGCCGCGTGGGCCAGTTCATAGGCGAAGCGCATGTTCCAGCGGTCCGAGCGC 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               144 GCCCCAGCCGCCATGCGGCCCTGTAGCGGCCCAAC-----GACGGC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 ArgProGlyGly---AlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAla 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 IleSerProGluAlaProValPro------ValValLysValAsnThrIleGluGlu 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgleuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeuAla 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 CGTGATGTAGGCGCGTAGGCGTCGCGAAACGCGCCGGCGTCGCTGACCAGGCGCTCGAA 43
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                                                                                                                                                                                                                                                                                                                       fragment of xylanase gene from degenerate primer amplification of soil DNA
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27
16
37
4
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 1998-08-06
PRIOR PADFLICATION NUMBER: 08/16,942
PRIOR FILING DATE: 1996-09-20
PRIOR FILING DATE: 1996-09-22
PRIOR FILING DATE: 1995-09-22
NUMBER OF SEQ ID NOS: 25
LENGTH: 294
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                                          22:
                                                                                                 TYPE: nucleic acid
STRANDEDNESS: DOUBLE
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                         318
61.00
45.74%
28.72%
2.55%
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                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Radomski, CCA APPLICANT: Seow, KT
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Query Match:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                             US-08-716-942-22
                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                  LENGTH:
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253 AlaGlnGluValTyrAspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAla 272
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225
336
423
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Matches:
Conservative:
Mismatches:
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                                                                                                            FILING DATE: AUGUST 8, 1992
ATTORNEY/AGENT INFORMATION:
NAME: William P. Berridge
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 28835A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6400
TELEFAX: (703) 836-5787
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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                     08/105,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mycobacterium chitae
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 268 base pairs
TYPE: nucleic acid
STRANDEDNESS: single-stranded
                                      FILING DATE: August 12, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR9210094
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 461-728
IDENTIFICATION METHOD:
OTHER INFORMATION:
PRIOR APPLICATION DATA:
                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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Best Local Similarity:
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ORIGINAL SOURCE:
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Patent No. 5849901

GENERAL INFORMATION:

APPLICANT: MABILAT et al.

TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET

TITLE OF INVENTION: WYCOBACTERIA

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Oliff & Berridge

STREET: 700 South Washington Street, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 AlaGlnGluValTyrAspValThrGlyAlaGlyAspThrValIleGlyValLeuAlaAla 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 ValValValGlyLysLeuGlyThrSerThrValSerProIleGluLeuGluAsnAlaVal 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 AlaAlaAlaArgLysArgGlyGluLysValValMetThrAsnGlyVal 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 GAGGTCGAGACCAAG-----GAGCAGATCGCCGCCACCGCCGGGATC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-912-020-325 (1-477) x US-08-105-168B-4 (1-268)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ength:
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                                                                                                                 ORGANISM: Mycobacterium chitae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS DOS 3.1
                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22314 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" DS/HD
COMPUTER: IBM COMPATIble
                                                                                                                                                                                                                                                                                  DENTIFICATION METHOD:
COTHER INFORMATION:
US-08-105-168B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                              INDIVIDUAL ISOLATE:
                                                                                                                                                                                    POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Alexandria,
STATE: Virginia
ZIP: 22314
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                  MAP POSITION:
FEATURE:
                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                     ANTI-SENSE
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                                                                                                                                    STRAIN:
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TELECOMMUNICATION INFORMATION
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98104-7092
                                                                                                                                                                                                                                                                                Best Local Similarity:
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                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                      Alignment Scores:
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APPLICANT:
APPLICANT:
APPLICANT:
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No
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         APPLICANT: GLIGAL, APAINED
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLECTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GROOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PATENTING DATE: 1998-04-16
SEQ ID NO 209
LENGTH: 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTAGTTGGGGCGGCGGCGGCGACTTCGCCGATTATCGCGACTGGCTGAAAGCCCGC--- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 LeuValGlyLeuThrGlyIleAspAspAla--------AlaArgAla 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 ArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAlaAsnAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/08818112

Patent No. 629069

GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
APPLICANT: Wedvick, Thomas S.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS
MUMBER OF SEQUENCES: 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 LeuSerLysSerLeuAlaAspValAşnValLysCysAspPheValSerVal 98
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20
20
119
16
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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6300 Columbia Center, 701 Fifth Avenue
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Matches:
Conservative:
Mismatches:
Indels:
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ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                      ; TYPE: DNA; ORGANISM: Mycobacterium tuberculosis
US-09-060-756-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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38.60%
35.09%
2.47%
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Washington
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Best Local Similarity:
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twacfack, Thomas S.
APPLICANT: Twacfack, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESSE: SED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
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24
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23
17
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 CGCGCCGCCAAGACCGCCGTTGCCGCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    326 GluGluLeuLysLeuAlaValAlaAla 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.08-818-111-37/c
Sequence 37, Application US/08818111
Patent No. 6338852
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Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TELEFAX: (206) 682-603 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            58.50
42.03%
34.78%
2.44%
                                                                   LENGTH: 290 base pairs:
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Abuna
STREET: bou
CITY: Seattle
Tome: Washington
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 ValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhe 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286 PheAlaAsnAlaAlaAlaGlyValValValGlyLysLeuGlyThrSerThrValSerPro
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APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Henditckson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
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                                                                                                                                                                                                                                                                                 Conservative:
Mismatches:
Indels:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-6031
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           Matches:
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Sequence 37, Application US/09072596
Patent No. 648836
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skeiky, Yasir A.W.
Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 05-MAY-1998 CLASSIFICATION:
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
              linear
                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
              ; TOPOLOGY:
US-09-056-556-37
                                                                                                                                                      Alignment Scores:
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                                                                                                                                                                                                                                                Score:
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| Fatent No. 6350456
| GENERAL INFORMATION:
| APPLICANT: Reed, Steven G. | APPLICANT: Reed, Steven G. | APPLICANT: Reed, Steven G. | APPLICANT: Bollon, Davin C. | TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 24 | CORRESPONDENCE ADDRESS: ADDRESSEE: SEED and BERRY LLP | STREET: 6300 Columbia Center, 701 Fifth Avenue | STREET: Gastle | State | S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 ValileGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhe 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 PhealaAsnAlaAlaAlaGlyValValValGlyLysLeuGlyThrSerThrValSerPro 305
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----CTGGCCACCTTACCGCC 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 | 111 | 111 | 111 | 112 | 111 | 112 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 113 | 
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION UNMER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEBYONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 ---GCCAATNCCGCC------
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INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 base pairs
TYPE: nucleic acid
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 37
SEQUENCE CHARACTERISTICS:
LENGTH: 290 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
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US-08-818-111-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
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Percent Similarity:
 US-08-818-112-39
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                                                                                                                                                                                                                                                                  286 PheAlaAsnAlaAlaGlyValValValValGlyLysLeuGlyThrSerThrValSerPro 305
                                                                                                                                                                                                                                                                                                                                                                                           306 IleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPheGlyValMetThrGlu 325
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sketky, Yasir A.W.
APPLICANT: Sketky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS.
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                      US-09-912-020-325 (1-477) x US-09-072-596-37 (1-290)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MAK1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.411C6
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 CGCGCCGCCAAGACCGCCGTTGCCGCC 135
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Patent No. 6290969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                     58.50
42.03%
34.78%
2.44%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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; TOPOLOGY: linear
US-09-072-596-37
                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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                                                    Alignment Scores:
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                                                                         Pred. No.:
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TUBERCULOSIS
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                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 148
CORRESPONDENCE SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                  155
15
7
18
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/818,111
FILING DATE: 13-MAR-1997
CLASSIPICATION: 4.24
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
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15
7
                                                       Conservative:
Mismatches:
Indels:
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                                                                                                                                                         US-09-912-020-325 (1-477) x US-08-818-112-39 (1-155)
                  Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39, Application US/08818111
Patent No. 6338852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285
57.50
53.66%
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LENGTH: 155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-818-111-39/c
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Pred. No.:
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Alignment Scores:
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TUBERCULOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 GlyAspThrValIleGlyValLeuAlaAlaThrLeu---AlaAlaGlyAsnSerLeuGlu 281
 282 GluAlaCysPhePheAlaAsnAlaAlaAlaGlyValValValGlyLysSLeuGlyThrSer 301
                                   æ
                         APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Campos-Neto, Antonia
APPLICANT: Wedvick, Thomas S.
APPLICANT: Twardalk, Daniel R.
APPLICANT: Hendrickson, Ronald C.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
WUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
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NAME: Maki, David J
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                    Sequence 39, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeik, Yasir A.W.
APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (206) 622-4900
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                  RESULT 15
US-09-072-596-39/c
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                                                                                                             263 GlyAspThrValIleGlyValLeuAlaAlaThrLeu---AlaAlaGlyAsnSerLeuGlu 281
                                                                                                                                       127 GGGGATACGACGGTGCCATTGTTCGACTCCGCGGTCCGGGGGTGCTGGCGAC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-056-556-39/c
Sequence 39, Application US/09056556
Fatent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                    155
15
7
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                        US-09-912-020-325 (1-477) x US-08-818-111-39 (1-155)
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 36.59%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104-7092
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Best Local Similarity:
Query Match:
 Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Seattle
                                                                                                                                                                                                                                                                302 Thr 302
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US-09-056-556-39
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Search completed: November 25, 2002, 01:01:12 Job time : 76 secs

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Sequence

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Sequence 285, App Sequence 7643, Ap Sequence 6039, Ap Sequence 11, App11 Sequence 2312, App Sequence 2010, App Sequence 2612, App Sequence 129, App Sequence 129, App Sequence 6038, App Sequence 6038, App Sequence 1225, App Sequence 1681, App Sequence 2614, App Sequence 2614, App Sequence 2614, App Sequence 2615, App Sequence 13171, App S
                                                           Sequence 159, App
Sequence 231, Ap
Sequence 253, Ap
Sequence 2568, Ap
Sequence 2568, Ap
Sequence 2768, Ap
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Sequence 1291, Ap
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APPLICANT: Porsyth, R. Allyn
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli
FILE REFERENCE: ELITHAR.009A;
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
US-09-974-300-6945
US-09-294-093B-4387
US-10-046-935-598
US-10-046-935-1291
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 89, Application US/09741669 Patent No. US20020022718A1
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US-09-741-669-89
    Percent Similarity:
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-WODEL-frame+ p2n.model -DEW-XIP
-Q-/Cgn2_1/USPTO_SPOO1/US0991202/Tunat_20112002_150301_11146/app_query.fasta_1.647
-Q-/Cgn2_1/USPTO_SPOO1/US0991202/Tunat_20112002_150301_11146/app_query.fasta_1.647
-DB-Published_Applications_NA -OFMN-fastap -SUFFIX-P2ns2Lm300_rnpb
-MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END-1
-MATRIX-blooun62 -TRANS-humand0.cdi -LIST-45 -DOCALIGN-200 -THR_SCRE-pct
-HRANIX-blooun62 -TRANS-humand0.cdi -LIST-45 -DOCALIGN-200 -THR_SCRE-pct
-HRANIX-bloon -ALINEN-0 -ALIST-300
-USER-US09912020_@CGN_1_147_@runat_20112002_150301_11146 -NCPU-6 -ICPU-3
-NO_XLDXY -NO_MMAP -LARGEQUERY -NEG_SCRES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 89, Appl
Sequence 1264, Ap
Sequence 5061, Ap
                                                                                                                                                          (without alignments)
2377.031 Million cell updates/sec
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                                                                                                                                                                                                                US-09-912-020-325
2393
1 MKVTLPEFERAGVMVVGDVM......FEDGCSTINIIKKIQQDKKG 477
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                                                                                                                                        November 24, 2002, 23:21:10 ; Search time 76 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/prodata/1/pubpna/USO7_PUBCOMB.seq:*
/cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/prodata/1/pubpna/NSO6_PUBM_PUB.seq:*
/cgn2_6/prodata/1/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/prodata/1/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/prodata/1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/prodata/1/pubpna/NSO8_NEW_PUB.seq:*
/cgn2_6/prodata/1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/prodata/1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/prodata/1/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/prodata/1/pubpna/USO9_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seg:*
                        GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                   nucleic search, using frame_plus_p2n model
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US-09-917-800A-1264
US-09-294-093B-5061
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                  335578 segs, 189365133 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                 Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 300
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                                                                                                                                                257 TyraspvalThrGlyalaGlyAspThrValIleGlyValLeualaAlaThrLeuAla--- 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Genbank Accession No. US20020119462A1 A1236089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Castle, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-05
CURRENT APPLICATION NUMBER: US,09/917,800A
CURRENT FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/290,629
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-12
PRIOR APPLICATION NUMBER: US 60/290,45
PRIOR FILING DATE: 2001-05-2
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-19
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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211 AAAAAGGC 203
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Best Local Similarity:
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US-09-917-800A-1264/c
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ORGANISM: Rattus
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                       Query Match:
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APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTURON: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 AlaAlaAlaArgLysArgGlyGluLysValValMetThrAsnGlyValPheAspIleLeu 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GGGCAGGCTCCTTCGCCAGGTGCTCGTGTTGTAGATGCAAGTTGATCTTTC 180
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218 GIGGACACCACGGGIGCIGGIGACAGITITIGIGGGAGCGCTTGCCITCTACCTGGCTTAC 159
                                           276 ---AlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaAlaGlyValVal 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                    158 TACCCAAGTCTGTCCTGGAAGAAATGCTCAAGAGATCTAATTCCATCGTGCGGTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               · LeuLysLeuAlaVal
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CTHER INFORMATION: Incyte ID NO. US20010051335A1 700355719H1

NAME/KEY: unsure

LOCATION: 83, 257, 263, 278

COTHER INFORMATION: a, t, c, 9, or other

US-09-294-093B-5061
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Conservative:
Mismatches:
Indels:
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                                                                                                                                295 ValGlyLysLeuGlyThrSerThrValSerPro 305
                                                                                                                                                                            98 GICCAGGCCACAGGAACACAGTCCTCTTATCCA 66
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US-09-878-574-10531
Sequence 10531, Application US/09878574
Patent No. US20020110548A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   Sequence 5061, Application US/09294093B Patent No. US20010051335A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GTATCTATGGACGACGNATCGANTCAG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 AlaValAsnSerAspAlaSerThrLys 381
                                                                                                                                                                                                                                                                                                                                    Lalgudi, Raghunath, V.
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Lal
                                                                                                                                                                                                                        RESULT 3
US-09-294-093B-5061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
SEQ ID NO 5061
LENGTH: 285
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Pred. No.:
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Sequence 159, Application US/09923876

Sequence 159, Application US/09923876

Sequence 159, Application US/09923876

Setent No. US20020013958A1

GENERAL INFORMATION:

APPLICANT: Lalgudi, Radhunath V.

APPLICANT: Calgudi, Radhunath V.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

TITLE OF INVENTION: PLOUD-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876

CURRENT PILING DATE: 1090-04-21

PRIOR FILING DATE: 1999-04-21

PRIOR PILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL PROGram
                                                                                                                                                            111 TTCGTCGGGAAGCTCGGCGACGACTTCGGGCACATGCTGCCCGGAATCCTGAAGGAG 170
                                                                                                                                                                                                                                       69 LeuValGlyLeuThrGlyIleAspAspAlaAlaArgAlaLeuSerLysSerLeuAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chisen, Rari L.
APPLICANT: Ohisen, Rari L.
APPLICANT: Ohisen, Rari L.
APPLICANT: Osykind, Judith W.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli
FILE REFERENCE: ELITRA 0009A
CURRENT APPLICATION NUMBER: US/09/741,669
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR RILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 481
SOFTWARE: FastSEQ for Windows Version 4.0
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Mismatches:
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Matches:
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; Sequence 90, Application US/09741669
; Patent No. US2002022718A1
; GENERAL INFORMATION:
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100.00%
2.93%
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US-09-741-669-90
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc_feature
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Best Local Similarity:
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US-09-923-876-159
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us-09-912-02.

APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: 105/09/878,574
CURRENT APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 10531
LENGTH: 263
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US-09-878-574-8726

Sequence 8725, Application US/09878574

Patent No. US2002011054841

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Thompson, Michael D.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(15401)B

CURRENT APPLICATION NUMBER: US/09/878,574

CURRENT FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 09/333,535

PRIOR PLIING DATE: 1999-06-14

NUMBER OF SEQ ID NOS: 15775

SEQ ID NO 8726

LENGTH: 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 GlnArgMetIleValLeuGlyAlaLeuGluAlaValAspTrpValVal 410
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
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Indels:
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ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 700966779H1
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COTHER INFORMATION: Clone ID: 701101576H1
US-09-878-574-8726
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92.00
58.93$
39.29$
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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Pred. No.:
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Pred. No.:
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RESULT 10
US-10-046-935-1960
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Sequence 3810, Application US/09294093B

Patent No. US2010051335A1

BERERL INFORMATION:
APPLICANT:
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TICALGANT:
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PARTICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 CCTGTGATCCTATTGCCC----AAGGAGAAGCTTGTTGACACCAACGGCGCAGGTGAC 124
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11 GTGATTACTCAAGGCGCTGATCCAGTGGTTGTTGCTGAGGATGGGAAGGTGAAAACGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 -----LeuHisMetProThrGlnAlaGlnGluValTyrAspValThrGlyAlaGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 ThrValIleGlyValLeuAlaAlaThrLeuAlaAlaGlyAsnSerLeuGluGluAlaCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 LeuValThrArgSerGluGlnGlyMetSerLeuLeuGlnProGlyLysAlaPro--
No. US20020013958A1 700156451H1
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                                                                                                                                                                                                                                Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                 US-09-912-020-325 (1-477) x US-09-923-876-159 (1-272)
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Conservative:
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Indels:
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; OTHER INFORMATION: Incyte ID
US-09-294-093B-3810
  Incyte ID
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69.00
48.00%
24.00%
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67.50
45.28%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
  OTHER INFORMATION:
                          NAME/KEY: unsure

LOCATION: 3

COTHER INFORMATION:

US-09-923-876-159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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                                                                                                                                                                                                Pred. No.:
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Molecules and Other Molecules Associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 AsnalaValArgGlyArgAlaAspThrGlyPheGlyValMetThrGluGluGluLeuLys 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 AspileLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArqLysLeuGlyAspArg 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 LeualaValalaalaAlaArgLysArgGlyGluLysValValMetThrAsnGlyValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 ATTGTAATGAGGCTT----AAACGATGGGAACGGAAGGAGTGTNNACCAAACAGCCTT
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27
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35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-024-Q1-B1-A3
US-09-878-574-2532
                       244 GCTTTTGATCTGTTCCATGCTGGACACGTCGAGATATTA 282
348 ValPheAspIleLeuHisAlaGlyHisValSerTyrLeu 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
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Indels:
                                                                         US-09-878-574-2532
US-09-878-574-2532
Sequence 2532, Application US/09878574
Parent No. US20020110548A1
GENERAL INFORMATION:
APPLICANT: BYTUM, JOSEPh R.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules a:
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
SEQ ID NO 2532
LEMCH: 281
LEMCH: 281
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Matches:
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Patent No. US20020156011A1
GENERAL INFORMATION:
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Secrist, Heather
Wang, Aijun
Stolk, John A.
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65.00
46.60%
26.21%
2.72%
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APPLICANT: Harlocker, Su
APPLICANT: Secrist, Heat
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A
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Best Local Similarity:
Query Match:
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Wed Nov 27 08:37:02,2002

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APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Ito, Laura, Y.
TYLE OF INVENTION: BEALDLEY, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL.
FILE REFERENCE: PL-0009 US
CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
SEQ ID NO 5568
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 AlaGlyValValValGlyLysLeuGlyThrSerThrValSerProlleGluLeuGluAsn 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 ATGGAATCCATGGTCCATGCAGACACAAGATCATTTATTCTGAAGAAGCCAAAGCTGTCT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 AlaValAlaAlaAlaArgLysArgGlyGluLysValValMetThrAsnGlyValPheAsp 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....--IleLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGly 367
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OTHER INFORMATION: Incyte ID No. US20010051335A1 700357413H1
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER FILE REFERENCE: 210121.5272.
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SEQ ID NO 1960
LENGTH: 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 AspArgLeuIleValAlaValAsnSerAspAlaSerThrLys 381
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Conservative:
Mismatches:
Indels:
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LOCATION: 18, 26, 235, 271
OTHER INFORMATION: a, t, c, g, or other
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64.00
39.36%
24.47%
2.67%
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                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-046-935-1960
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Best Local Similarity:
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Pred. No.:
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
APPLICANT: Chen, Wensheng
APPLICANT: Chen, WENSHENG
APPLICANT: Chen, WENSHENG
APPLICANT: CHEN WENSHENG
APPLICANT: CHENE CHENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                              297 CCAATCAGCAGGGCCCTCGGGGAACCNCAGGGCAATCTCCTTATTAGCACTCTCAATGCT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                          237 GINAAITCCAIGAAIGACAITCCIGCCAAIGICGACAGCAAAGICGCCACGGAIGGIGCC 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 LysLeuArgValLeuSerArgAsnGlnGlnLeuIleArgLeuAspPheGluGluGlyPhe 125
                                                                                                                                                                                                                                                    28 ProThrSerArgIle-----SerProGluAlaProValValLySValAsnThr 45
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                                                                                                                                                                                                                                                                                                                                                                            46 IleGluGluArgProGlyGlyAlaAlaAsnValAlaMetAsnIleAlaSerLeuGlyAla
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                                   Conservative:
                                                             Mismatches:
      Matches:
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2001-01-07
PRIOR PILING DATE: 2001-01-07
PRIOR PELICATION NUMBER: PCT/US01/00666
PRIOR PILING DATE: 2001-01-30
                                                                                              Indels:
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PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 27168, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
64.00
37.50%
24.04%
2.67%
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                                Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-912-020-325 (1-477) x US-09-954-531-285 (1-176)
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LENGTH: 176
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Sequence 729, Application US/09923876

Patent No. US20020013958A1

GENERAL INFORMATION:

APPLICANT: Lalqudi, Raghunath V.

APPLICANT: Lalqudi, Raghunath V.

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923,876

CURRENT FILING DATE: 1999-06-05

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-06-05

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL PROGRAM
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                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: MAP TO ALL21760.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.99
OTHER INFORMATION: SMISSPROT HIT: 049075, EVALUE 1.40e+00
OTHER INFORMATION: NT HIT: U69097.1, EVALUE 5.50e-01
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: DC10-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-06-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 27168
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Matches:
Conservative:
Mismatches:
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63.50
44.44%
28.40%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
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Sequence 285, Application US/09954531

Sequence 285, Application US/09954531

Patent No. US20020165180A1

GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Gene Sets
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689209-77

CURRENT FILING DATE: 2002-05-02

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR PILING DATE: 2000-09-20

PRIOR PILING DATE: 2000-09-22

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 LeuAlaAlaGlyAsnSerLeuGluGluAlaCysPhePheAlaAsnAlaAlaGlyVal
                                                                                                            NAME/KEY: misc_feature

CTHER INFORMATION: Incyte ID No. US20020013958A1 700157457H1

NAME/KEY: USBURE

LOCATION: 44, 266

COTHER INFORMATION: a, t, c, g, or other

US-09-923-876-729
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Mismatches:
Indels:
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Mismatches:
Indels:
Gaps:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 ValValGlyLysLeuGly 299
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63.00
50.00%
28.26%
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; ORGANISM: Homo sapiens
US-09-954-531-285
SEQ ID NO 729
LENGTH: 268
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
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Query Match:
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US-09-954-531-285
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350 AsplieLeuHisAlaGlyHisValSerTyrLeuAlaAsnAlaArgLysLeuGlyAspArg 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 ProlleGluLeuGluAsnAlaValArgGlyArgAlaAspThrGlyPheGlyValMetThr 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TTGGCA 153
                                 3 GATTIGCCAATGCATAACAGGGTTTCAATTCATTAATGAAGGGACTCAATCGCCTAGA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::::: ||| :::|||
7 TCAATCAAAGGAAAAGTGGCGCTTATTACAGGAGCTGGACGTGGAATTGGCCGTGCTGCA 66
                                                                                                                                                                                                     us-09-974-300-7643

is Sequence 7643.

sequence 7643.

sequence 7643.

patent No. US20020146721A1

ig GENERAL INFORMATION:

APPLICANT: Clausen, Ib Groth

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OF INVENTION: Expression

FILE REPERENCE: 10085.500-US

CURRENT APPLICATION NUMBER: US/09/974,300

CURRENT APPLICATION NUMBER: US/09/974,300

PRIOR FILING DATE: 2001-10-05

PRIOR FILING DATE: 2001-10-05

PRIOR FILING DATE: 2001-03-27

NUMBER: OF SEQ ID NOS: 8481

SOFTWARE: FESTSEQ for Windows Version 4.0

SEQ ID NO 7643

LENGTH: 234
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                         123 CTTGGACCGTGGAATTCACATTTCATATTCTTG 155
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60.50
46.48%
29.58%
2.53%
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US-09-974-300-7643
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Best Local Similarity:
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Search completed: November 25, 2002, 01:02:42 Job time : 78 secs

